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U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. 371**

001560-373

U.S. APPLICATION NO. (If known, see 37 C.F.R. 1.5)

09/402093INTERNATIONAL APPLICATION NO.
PCT/JP99/00406INTERNATIONAL FILING DATE
January 29, 1999PRIORITY DATE CLAIMED
January 30, 1998 ✓

TITLE OF INVENTION
PROCESS FOR PRODUCING PEPTIDES USING A HELPER PEPTIDE

APPLICANT(S) FOR DO/EO/US

Kazuhiro OHSUYE, Masayuki YABUTA, Yuji SUZUKI ✓

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and the PCT Articles 22 and 39(1).
4. ☐ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
6. ☒ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern other document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☒ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☒ A **FIRST** preliminary amendment.
☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information:

International Search Report; Preliminary Examination Report; PCT Demand, Sequence Listing, Declaration and Disk

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U.S. APPLICATION NO. 09/402093		INTERNATIONAL APPLICATION NO. PCT/JP99/00406		ATTORNEY'S DOCKET NUMBER 001560-373	
17. <input checked="" type="checkbox"/> The following fees are submitted:				CALCULATIONS	PTO USE ONLY
Basic National Fee (37 CFR 1.492(a)(1)-(5)): Search Report has been prepared by the EPO or JPO \$840.00 International preliminary examination fee paid to USPTO (37 CFR 1.482) \$670.00 No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)) \$780.00 Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$970.00 International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4) \$96.00					
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$ 970.00	
Surcharge of \$130.00 for furnishing the oath or declaration later than months from the earliest claimed priority date (37 CFR 1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30				\$	
Claims	Number Filed	Number Extra	Rate		
Total Claims	27 - 20 =	7	X\$18.00	\$ 126.00	
Independent Claims	3 - 3 =	0	X\$78.00	\$ 0	
Multiple dependent claim(s) (if applicable)			+0\$260.00	\$ 0	
TOTAL OF ABOVE CALCULATIONS =				\$ 1,096.00	
Reduction for 1/2 for filing by small entity, if applicable. Verified Small Entity statement must also be filed. (Note 37 CFR 1.9, 1.27, 1.28).				\$ 0	
SUBTOTAL =				\$ 1,096.00	
Processing fee of \$130.00 for furnishing the English translation later than months from the earliest claimed priority date (37 CFR 1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30				\$ 0	
TOTAL NATIONAL FEE =				\$ 1,096.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property +				\$ 40.00	
TOTAL FEES ENCLOSED =				\$ 1,136.00	
				Amount to be refunded	\$
				charged	\$

a. ☒ A check in the amount of \$ 1,136.00 to cover the above fees is enclosed.b. ☐ Please charge my Deposit Account No. 02-4800 in the amount of \$ to cover the above fees. A duplicate copy of this sheet is enclosed.c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 02-4800. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

SIGNATURE

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REGISTRATION NUMBER 36.607

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Patent
Attorney's Docket No. 001560-373

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of)
)
Kazuhiro OHSUYE et al) Group Art Unit: Unassigned
)
Application No.: Unassigned) Examiner: Unassigned
Corresponding to PCT/JP99/00406)
)
Filed: September 29, 1999)
)
For: PROCESS FOR PRODUCING)
PEPTIDES USING A HELPER)
PEPTIDE)

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Prior to examination on the merits, please amend the above-identified application as follows:

IN THE SPECIFICATION:

Please insert the enclosed Sequence Listing before the claims and renumber the pages accordingly.

IN THE CLAIMS:

Please amend claims as follows:

In claim 3, line 1, please delete "or 2."

In claim 4, line 1, please delete "any of claims 1 to 3" and insert in place thereof

--claim 1--.

In claim 5, line 1, please delete “any of claims 1 to 4” and insert in place thereof

--claim 1--.

In claim 6, line 1, please delete “any of claims 1 to 5” and insert in place thereof

--claim 1--.

In claim 8, line 1, please delete “any of claims 1 to 5” and insert in place thereof

--claim 1--.

In claim 9, line 1, please delete “any of claims 1 to 8” and insert in place thereof

--claim 1--.

In claim 10, line 1, please delete “any of claims 1 to 9” and insert in place thereof

--claim 1--.

In claim 12, line 1, please delete “any of claims 1 to 11” and insert in place thereof --
claim 1--.

In claim 13, line 1, please delete “any of claims 1 to 11” and insert in place thereof --
claim 1--.

In claim 14, line 1, please delete “any of claims 1 to 11” and insert in place thereof --
claim 1--.

In claim 16, line 1, please delete “or 15.”

In claim 17, line 1, please delete “or 15.”

In claim 18, lines 1-2, please delete “any of claims 12 to 17” and insert in place

thereof --claim 12--.

In claim 20, lines 1-2, please delete “any of claims 12 to 17” and insert in place thereof --claim 12--.

In claim 21, lines 1-2, please delete “any of claims 12 to 17” and insert in place thereof --claim 12--.

In claim 22, lines 1-2, please delete “any of claims 14 to 21” and insert in place thereof --claim 14--.

In claim 23, line 1, please delete “any of claims 1 to 22” and insert in place thereof --claim 1--.

In claim 24, lines 4-5, please delete “any of claims 14 to 23” and insert in place thereof --claim 14--.

REMARKS

Entry of the foregoing and examination of the above-identified application is respectfully requested.

The specification has been amended to insert the Sequence Listing before the claims. It is respectfully requested that the pages be renumbered accordingly. No new matter is being added by this Sequence Listing.


The claims have been amended to delete multiple dependencies.

Early and favorable action in the form of a Notice of Allowance is respectfully requested and believed to be in order.

In the event that there are any questions relating to this amendment or the application in general, it would be appreciated if the Examiner would contact the undersigned attorney at the number identified below to expedite prosecution of this application.

Respectfully submitted,

BURNS, DOANE, SWECKER & MATHIS, L.L.P.

By:  #39,300
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Date: September 29, 1999

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STY-F962/PCT

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DESCRIPTION

PROCESS FOR PRODUCING PEPTIDES USING A HELPER PEPTIDE

Technical Field

5 The present invention relates to a process for
producing peptides using genetic engineering technology.
Background Art

10 Many biologically active peptides have been produced
by genetic engineering technology using microorganisms,
animal cells, and the like as hosts. As processes for
producing a peptide of interest, there are known so-
called direct expression method such as a process for
extracellularly secreting a peptide, or a process for
expressing a peptide from the N-terminal in the cell; or
15 a process for expressing a fusion protein in which a
protective peptide has been added to the N-terminal or
the C-terminal of the peptide, or the like. Processes
have been used wherein a peptide of interest is expressed
either inside or outside of the cell, the expression
20 product is then subjected to chemical or enzymatic
cleavage or modification to produce the peptide of
interest, which is then purified in a purification
process to yield the peptide.

25 For the production of low molecular weight peptides,
the fusion protein expression process mentioned above is
generally used in order to avoid degradation of the
protein by intracellular proteolytic enzymes. In this
case, processes have been used wherein after
intracellular expression of a fusion protein having a
30 cleavage site region added thereto in between the peptide
of interest and the protective peptide said cleavage site
region being designed so as to permit cleavage by a
chemical or enzymatic reaction, the peptide of interest
is cleaved from the fusion protein by a chemical or
35 enzymatic means, and the peptide is isolated and purified
by a precipitation or a chromatographic process.

Furthermore, when the protein of interest is a

protein of which a C-terminal has been amidated, such as calcitonin, a peptide having a glycine residue added to the C-terminal end of said peptide is expressed as a part of a fusion protein, the glycine-extended peptide of interest is cleaved from the fusion protein by a proteolytic enzyme, an amidating enzyme which is a modification enzyme is allowed to act on the peptide to produce an amidated peptide, and the amidated peptide of interest is obtained through purification processes.

However, when the production of peptides on an industrial scale is desired, various problems may arise as to the solubility and gelling of the peptide of interest in various conditions for cleaving and modification reactions, the concentration of a sample to be loaded to the column in the chromatographic process, the elution condition from the column, stability after elution, and the like. Most of the problems are caused by various physicochemical properties of the peptide of interest.

As the peptide of interest, for example, there can be mentioned human glucagon-like peptide-1 (referred to hereinafter as GLP-1; Bell GI et al., Nature, Vol. 304, pp. 368-371, 1983) and derivatives of GLP-1 (referred to hereinafter as GLP-1 derivatives) having an insulintropic activity. GLP-1 is a peptide consisting of 37 amino acid residues derived from preproglucagon. Through processing of preproglucagon, GLP-1(7-37) in which 6 amino acids at the N-terminal of GLP-1 are deleted and GLP-1(7-36)NH₂ in which the C-terminal of GLP-1(7-36) has been modified to an amide form have been biosynthesized (Mojsow, S. et al., J. Clin. Invest. Vol. 79, pp. 616-619, 1987). Since these peptide hormones have an activity of promoting the secretion of insulin by acting on the beta cells in the pancreas, the possibility as candidates of a therapeutic agent for diabetics has been proposed based on their pharmacological effects in recent years (Gutniak M. K., et al., New England

Medicine, Vol. 326, pp. 1316-1322, 1992; Nathan D. M., et al., Diabetes Care, Vol. 15, pp. 270-275, 1992).

5 As a process for producing the above peptide, a case may be contemplated in which the peptide is produced by a fusion protein expression method using E. coli etc. as a host in the conventional method mentioned above. In the case of GLP-1(7-37), for example, it is expressed as a fusion protein in which a protective peptide is added to the N-terminal or C-terminal end of GLP-1(7-37) through a
10 cleavage site region for excising out GLP-1(7-37) from the fusion protein either chemically or enzymatically, and then GLP-1(7-37) can be excised out from the fusion protein either chemically or enzymatically to produce GLP-1(7-37). And, GLP-1(7-36)NH₂ can be produced by
15 adding a step of modification reaction to the above process. Thus, GLP-1(7-37) is expressed as a fusion protein as mentioned above as a substrate for an amidation enzyme for the amidation modification reaction wherein GLP-1(7-37) can be considered as an intermediate
20 peptide for the production of GLP-1(7-36)NH₂. GLP-1(7-37) is excised from the fusion protein either chemically or enzymatically, and then the GLP-1(7-37) thus obtained is subjected to an amidation modification reaction using an amidation enzyme to produce the desired GLP-1(7-
25 36)NH₂.

However, even when the above mentioned processes are used to produce a peptide of interest, a GLP-1 derivative having an insulinotropic activity, undesirable problems on production processes arise. Therefore, production
30 processes that permit inexpensive supply on an industrial level have not been established yet, and thus there is a strong need for the establishment of such methods.

For example, as a process for producing GLP-1(7-37) as a peptide of interest a fusion protein comprising a
35 protective peptide and GLP-1(7-37) is expressed in a conventional process, as mentioned above, and GLP-1(7-37) can be produced by excising it directly from said

protein. Thus, the purification steps of the production process can use (1) enzymatic excision step of GLP-1(7-37) from the fusion protein and (2) a chromatographic step. However, since GLP-1(7-37) can easily gel or aggregate during purification, problems on production processes that are derived from physicochemical properties, such as markedly reduced recovery and incapability of resin regeneration, may sometimes arise. Once it has been gelled, though it can be solubilized at pH 10 or higher and can be purified, problems such as undesirable modifications and conformational changes may appear (Senderoff RI, et al., J. Pharm. Sci., Vol. 87, pp. 183-189, 1998).

Furthermore, when the peptide of interest is an amidated peptide GLP-1(7-36)NH₂, problems may arise as to the amidation reaction. Thus, optimal pH of enzymatic amidation reactions is approximately from weak acid to neutral, whereas the theoretical isoelectric points of GLP-1(7-37) and GLP-1(7-36)NH₂ are pI = 5.5 and pI = 7.5, respectively. Therefore, when an enzymatic conversion to GLP-1(7-37) is carried out at the optimal pH of an amidation enzyme that is near the isoelectric point of the substrate GLP-1(7-37), it is believed that GLP-1(7-37) tends to form an isoelectric precipitation.

Furthermore, since GLP-1(7-36)NH₂ that was formed by the precipitated GLP-1(7-37) also coprecipitates, enzyme reactions may not fully proceed causing problems in production processes. Furthermore, since GLP-1(7-36) is also a peptide that tends to aggregate in handling during the column step and to gel in the column, problems as to purification may also arise. Thus, it is expected that GLP-1 derivatives also have the above-mentioned problems, in production processes, that are derived from physicochemical properties.

In the production of GLP-1(7-37), GLP-1(7-36)NH₂ and GLP-1 derivatives on an industrial scale, the above-mentioned problems can cause problems on industrial

production derived from the physicochemical properties of the peptide of interest itself, causing serious problems in terms of yield, process control, and even production cost.

5 Disclosure of the Invention

It is an object of the present invention to provide a process for producing a peptide of interest in an efficient manner by relieving the problems derived from the physicochemical properties of the peptide of interest
10 itself (for example, the problem of low solubility and gelling in the chemical and enzymatic reaction or the purification step in the production processes of the peptide of interest), when an efficient production of said peptide of interest on an industrial scale using
15 genetic engineering technology is contemplated.

The term "the peptide of interest of the present invention" as used herein means not only the peptide finally obtained but also the production intermediate peptides that are required in the production process
20 thereof.

In order to avoid the above-mentioned problems, the inventors of the present invention have found a process for producing a peptide of interest in an efficient manner by relieving the problems of the peptide of
25 interest by adding a helper peptide to the peptide of interest. Thus, the process for producing a peptide claimed in the present invention is a method for producing a peptide having the desired biological activity, said method comprising the steps of:

30 (1) culturing cells transformed with an expression vector having the nucleotide sequence encoding the peptide of interest that has a helper peptide added thereto or a fusion protein that has a protective peptide further added to the peptide of interest that has a
35 helper peptide added thereto, and then harvesting said peptide of interest that has a helper peptide added thereto or said fusion protein, from said culture;

(2) in the case wherein a fusion protein is obtained in step (1), cleaving off from said fusion protein the peptide of interest that has a helper peptide added thereto and the protective peptide, and purifying the peptide of interest that has a helper peptide added thereto as desired;

(3) in the case wherein modification is required for the peptide of interest, subjecting the peptide of interest that has a helper peptide added thereto obtained in step (1) or step (2) to a modification reaction;

(4) cleaving off from the peptide of interest that has a helper peptide added thereto obtained in step (1), step (2) or step (3), the helper peptide and the peptide of interest, and purifying the peptide of interest as desired; and

(5) purifying the peptide of interest obtained in step (4) (Figure 1).

Brief Description of Drawings

Figure 1 outlines a process for producing the peptide of interest using a helper peptide.

Figure 2 is a drawing that shows a process for constructing pG117S4HR6GLP-1.

Figure 3 is a drawing that shows a process for constructing pGP117S4HompRHKR.

Figure 4 is a drawing that shows a process for constructing pGP117S4HompRHPR.

Figure 5 is a drawing that shows a process for constructing pGP97ompPR.

Figure 6 is a drawing that shows the oligonucleotides and the primers used for constructing pGP97ompPR.

Figure 7 is a drawing that shows an amino acid sequence of a fusion protein (GP97ompPR) encoded by pGP97ompPR. The underlined part indicates the amino acid sequence derived from GLP-1(7-37), and the double-underlined part indicates the sequence of a helper peptide. ↓ indicates the cleavage site by the E. coli

OmpT protease, and the arrow after the double-underline indicates the cleavage site by Kex2 protease.

5 Figure 8 is a drawing that shows the nucleotide sequence of DNA of a fusion protein (GP97ompPR) encoded by pG97ompPR, wherein the region from A of the nucleotide number 1 to T of the nucleotide number 462 encodes the fusion protein of GLP-1(7-37). lac PO represents the promoter/operator region of the E. coli lactose operon.

10 Figure 9 is a photograph of an electrophoresis that shows the culturing of a recombinant E. coli cells and an expression of a fusion protein (GP97ompPR). In the figure are shown the results of the SDS-polyacrylamide gel electrophoresis of the samples at sampling times a through e. The arrow in the figure indicates the band of the fusion protein.

15 Figure 10 is a drawing that shows an analysis of the cleavage of a fusion protein (GP97ompPR) with the E. coli OmpT protease present in the inclusion bodies.

20 Figure 11 is a drawing that shows an amino acid sequence of a fusion protein encoded by pG117S4HR6GLP-1. In the figure, the underlined part indicates an amino acid sequence derived from GLP-1(7-37), and the double-underlined part indicates an amino acid sequence derived from a helper peptide.

25 Figure 12 is a drawing that shows an amino acid sequence of a fusion protein encoded by pGP117S4HomprHHR. In the figure, the underlined part indicates an amino acid sequence derived from GLP-1(7-37), and the double-underlined part indicates an amino acid sequence derived from a helper peptide.

30 Figure 13 is a drawing that shows an amino acid sequence of a fusion protein encoded by pGP117S4HomprHPR. In the figure, the underlined part indicates an amino acid sequence derived from GLP-1(7-37), and the double-underlined part indicates an amino acid sequence derived from a helper peptide.

35 Figure 14 is a drawing that shows an elution pattern

of RHHGP[G] from the SP Sepharose Big beads, wherein the starting position of elution is shown by ↓ and the pooled fractions are shown in the figure. Absorbance was measured at 280 nm.

5 Figure 15 is a drawing that shows an analytical pattern at each purification step in the cleavage process of GLP-1(7-37) from RHHGP[G] by Kex2 protease. In the figure, A indicates a reverse-phase pool before cleavage with Kex2 protease, B after cleavage with the Kex2
10 protease, and C after PorosR2, and 1 indicates RHHGP[G] and 2 indicates GLP-1(7-37).

Figure 16 is a drawing that shows the pH dependency of the amidation reaction of RHHGP[G].

15 Figure 17 is a drawing that shows a time course of the conversion of RHHGP[G] to RHHGP-1 in an amidation reaction as measured by an ion exchange HPLC, wherein 1 indicates RHHGP[G] and 2 indicates RHHGP-1. Absorbance was measured at 280 nm.

The analytical condition was as follows:

20 Column: Poros S/H, 4.6 mm I.D. × 50 mm

Flow rate: 1.6 ml/min

Solution A: 30 mM BR buffer, pH 6.0

Solution B: 30 mM BR buffer, pH 9.0

Equilibration: solution A

25 Elution: solution B 0% → 100%, linear pH gradient.

Figure 18 is a drawing that shows the pH dependency of a Kex2 protease processing reaction with RHHGP-1 as a substrate.

30 Figure 19 is a drawing that shows an elution pattern and a pH gradient created, in the purification of GLP-1(7-36)NH₂ by Macrorep High-S. Absorbance was measured at 280 nm.

35 Figure 20 is a drawing that shows the removal of impurities with Macrorep High-S, wherein A indicates the sample loaded to the column, B indicates an analytical HPLC pattern. 1 indicates GLP-1(7-37) and 2 indicates

GLP-1(7-36) NH₂. Absorbance was measured at 280 nm.

Figure 21 is a drawing that collectively shows the analytical HPLC patterns of samples in each purification process in the production of GLP-1(7-36)NH₂ through the first cleavage with OmpT and the second cleavage with Kex2 protease. A indicates a reverse-phase HPLC pattern after OmpT, B after SP Sepharose, C after Kex2 reaction, D after Macroprep High-S, and E after Poros R2. 1 indicates GP97ompPR, 2 indicates the protective peptide, 3 indicates RHHGP[G], 4 indicates RHHGP-1, and 5 indicates GLP-1(7-36) NH₂. Absorbance was measured at 280 nm.

The analytical condition was as follows:

Column: YMC Protein RP, 4.6 mm I.D. × 50 mm

Flow rate: 1.0 ml/min

Solution A: 0.1% TFA / 10% acetonitrile

Solution B: 0.1% TFA / 60% acetonitrile

Equilibration: solution A

Elution: solution B 44% → 74% /12 min.

Figure 22 is a drawing that shows the pH dependency of the solubility of RHHGP[G], RHHGP-1, GLP-1(7-37), and GLP-1(7-36)NH₂.

Figure 23 is a drawing that shows a suppressing effect on the aggregation of RHHGP[G], RHHGP-1, and GLP-1(7-36)NH₂ by Tween 80, wherein A indicates the suppression of aggregation of RHHGP[G] and RHHGP-1 by Tween 80, and B indicates the suppression of aggregation of GLP-1(7-36)NH₂ by Tween 80.

Figure 24 is a drawing that shows a suppressing effect on the aggregation of GLP-1(7-36)NH₂ by NaCl and temperature, wherein C indicates the suppression of aggregation of GLP-1[G] by NaCl and D indicates the suppression of aggregation of GLP-1(7-36)NH₂ by temperature.

Embodiments for Carrying Out the Invention

The helper peptide according to the present

invention is a peptide that is used to circumvent the problems on industrial production derived from physicochemical properties of the peptide of interest itself. Of the problems on industrial production derived from physicochemical properties of the peptide of interest itself, special attention is paid to the problem in chemical or enzymatic reactions and purification during the production process of said peptide, such as problems of solubility and gelling of the peptide of interest under various conditions of cleavage and modification reactions, the problem of sample concentration to be loaded on the column during the column chromatographic process, the problem of the elution conditions from the column and the stability after elution, and the like.

The helper peptide of the present invention may be prepared as appropriate depending on the physicochemical properties of the peptide of interest. For example, when the isoelectric point of the peptide of interest is neutral to weak acid and the optimum pH during the production process is also neutral to weak acid and thereby the solubility of the peptide of interest under such pH is too low, then the helper peptide is preferably designed so that the isoelectric point (pI) of the peptide of interest that has a helper peptide added thereto is 8 to 12 and more preferably 9 to 11. The helper peptide of the present invention may be added to either the N-terminal or C-terminal of the peptide of interest. The dimension (length) of a helper peptide is preferably 5 to 50 amino acid residues, and more preferably from 5 to not greater than 30 amino acid residues, but it contains at least one basic amino acid or acidic amino acid.

In addition to the above-mentioned GLP-1 derivatives, the peptides of interest that can be produced according to the present invention include , but are not limited to, the peptides comprising not greater

than 200 amino acid residues. Examples of such peptides include adrenocorticotrophic hormone, adrenomedullin, amylin, angiotensin I, angiotensin II, angiotensin III, A-type natriuretic peptide, B-type natriuretic peptide, 5 bradykinin, big gastrin, calcitonin, calcitonin gene related peptide, cholecystokinin, corticotropin releasing factor, cortistatin, C-type natriuretic peptide, defesin 1, delta sleep-inducing peptide, dynorphin, elafin, α -endorphin, β -endorphin, γ -endorphin, endothelin-1, 10 endothelin-2, endothelin-3, big endothelin-1, big endothelin-2, big endothelin-3, enkephalin, galanin, big gastrin, gastrin, gastric inhibitory polypeptide (GIP), gastrin releasing peptide, glucagon, glucagon-like peptide-2, growth hormone releasing factor, growth 15 hormone, guanylin, uroguanylin, histatin 5, insulin, joining peptide, luteinizing hormone releasing hormone, melanocyte stimulating hormone, midkine, motilin, neurokinin A, neurokinin B, neuromedin B, neuromedin C, neuropeptide Y, neurotensin, oxytocin, proadrenomedullin 20 N-terminal 20 peptide, cromogranin A, parathyroid hormone, PTH related peptide, peptide histidine-methionine-27, pituitary adenylate cyclase activating polypeptide 38, platelet factor-4, peptide T, secretin, serum thymic factor, somatostatin, substance P, 25 thyrotropin releasing hormone, urocortin, vasoactive intestinal peptide, vasopressin, and the derivatives thereof, etc.

As the GLP-1 derivatives, in addition to the above-mentioned GLP-1(7-37) and GLP-1(7-36)NH₂, there can be 30 mentioned peptides having an insulinotropic activity in which amino acid residues have been substituted for, added to, and/or deleted from the peptide comprising 37 amino acid residues of GLP-1, peptides having an insulinotropic activity in which amino acids of said 35 peptide have been further modified (for example an amidated form), and peptides having an insulinotropic

activity that are obtained from the combinations thereof.

Furthermore, as the GLP-1 derivatives that are suitably produced according to the method of the present invention, those GLP-1 derivatives that have isoelectric points from 4.5 to 9.0 are preferred. More preferably they are GLP-1 derivatives having isoelectric points from 5.5 to 7.5.

As the GLP-1 derivatives, in addition to those mentioned above, the following can be mentioned:

GLP-1(7-34), GLP-1(7-35), GLP-1(7-36), GLP-1(7-34)NH₂, GLP-1(7-35)NH₂, and GLP-1(7-37)NH₂;

GLP-1(7-37)-Arg, GLP-1(7-37)-Arg-Arg, GLP-1(7-37)-Lys, GLP-1(7-37)-Lys-Lys, GLP-1(7-37)-Lys-Arg, and GLP-1(7-37)-Arg-Lys, and the C-terminal-amidated forms thereof;

GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 8, Ala, of GLP-1 has been substituted with Thr, Gly or Ser;

GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 26, Lys, of GLP-1 has been substituted with Arg;

GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 34, Lys, of GLP-1 has been substituted with Arg;

GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 36, Arg, of GLP-1 has been substituted with Lys;

GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 8, Ala, of GLP-1 has been substituted with Thr, Gly or Ser, and the amino acid at position 26, Lys, has been substituted with Arg;

GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 8, Ala, of GLP-1 has been substituted with Thr, Gly or Ser, and the amino acid at position 34, Lys, has been substituted with Arg;

GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 8, Ala, of GLP-1 has been substituted

with Thr, Gly or Ser, and the amino acid at position 36, Arg, has been substituted with Lys;

5 GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 26, Lys, of GLP-1 has been substituted with Arg, and the amino acid at position 34, Lys, has been substituted with Arg;

10 GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 26, Lys, of GLP-1 has been substituted with Arg, and the amino acid at position 36, Arg, has been substituted with Lys;

15 GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 34, Lys, of GLP-1 has been substituted with Arg, and the amino acid at position 36, Arg, has been substituted with Lys;

20 GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 8, Ala, of GLP-1 has been substituted with Thr, Gly or Ser, the amino acid at position 26, Lys, of GLP-1 has been substituted with Arg, and the amino acid at position 34, Lys, has been substituted with Arg;

25 GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 8, Ala, of GLP-1 has been substituted with Thr, Gly or Ser, the amino acid at position 26, Lys, of GLP-1 has been substituted with Arg, and the amino acid at position 36, Arg, has been substituted with Lys;

30 GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 8, Ala, of GLP-1 has been substituted with Thr, Gly or Ser, the amino acid at position 34, Lys, of GLP-1 has been substituted with Arg, and the amino acid at position 36, Arg, has been substituted with Lys;

35 GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 26, Lys, of GLP-1 has been substituted with Arg, the amino acid at position 34, Lys, of GLP-1 has been substituted with Arg, and the amino acid at position 36, Arg, has been substituted with Lys; and

GLP-1(7-37) and GLP-1(7-36)NH₂ in which the amino acid at position 8, Ala, of GLP-1 has been substituted with Thr, Gly or Ser, the amino acid at position 26, Lys,

of GLP-1 has been substituted with Arg, and the amino acid at position 36, Arg, has been substituted with Lys.

In the case of GLP-1(7-37) as an example of the peptide of interest, a helper peptide having basic amino acids can be added to GLP-1(7-37) and then can be used for the production of GLP-1(7-37) in order to relieve the problems on purification processes such as the gelling and the solubility of GLP-1(7-37). Thus, by adding the helper peptide to GLP-1(7-37), the isoelectric point ($pI = 5.5$) of GLP-1(7-37) can be shifted to the alkali side and thereby the hydrophilicity can be increased so as to avoid the problems on purification processes such as aggregation (gelling) in the column. Furthermore, by adding said helper peptide to GLP-1(7-37), it has become possible to isolate a peptide comprising the helper peptide and GLP-1(7-37) at very high purity and high yields in the first chromatographic process, which results in enhanced recovery of GLP-1(7-37), indicating that the use of a helper peptide is very useful in this process.

In the case of GLP-1(7-36)NH₂ as an example of the peptide of interest, it is necessary to first obtain an intermediate product (said peptide is specifically GLP-1(7-37)) as the peptide of interest since GLP-1(7-36)NH₂ is an amidated peptide. Thus, a helper peptide having a basic amino acid can be added to GLP-1(7-37), which can be used for the production of GLP-1(7-36)NH₂. By adding a helper peptide having a basic amino acid, the isoelectric point of GLP-1(7-37) can be shifted to the alkali side and thereby precipitate formation can be suppressed due to increased solubility of the peptide having a helper peptide added to GLP-1(7-37) at the pH of the amidation enzymatic reaction liquid at a subsequent amidation modification reaction and thereby the recovery and the yield can be increased. By adding a hydrophilic helper peptide containing a basic amino acid, the solubility of the peptide of interest can also be

increased, and furthermore the aggregation of GLP-1(7-37) as the substrate in the amidation modification reaction and GLP-1(7-36)NH₂ as a product can be avoided, thereby indicating that the addition is very useful in the purification process after the amidation enzymatic reaction.

In any of the above cases, the peptide having a helper peptide added to GLP-1(7-37) has preferably an isoelectric point of 8 to 12. By subjecting said peptide to the action of a cation ion exchange resin, said peptide can be obtained at high yields (98% or greater).

In order to obtain the peptide of interest from the peptide that has a helper peptide added thereto, a cleavage site region is introduced that permits chemical or enzymatic cleavage in between the helper peptide and the peptide of interest. For the cleavage site region as well, a cleavage site region having a high cleavage efficiency is designed depending on the physicochemical properties owned by the peptide of interest. As the enzymatic and chemical cleavage methods, those described in Methods in ENZYMOLOGY, Vol. 185, Gene Expression Technology (David V. Goeddel ed., published by ACADEMIC PRESS, INC.) can also be used.

As the chemical cleavage method, there can be mentioned a method in which the C-terminal end of methionine is cleaved with cyanogen bromide (D. V. Goeddel et al., Proc. Natl. Acad. Sci. U.S.A., Vol. 76, pp. 106-110, 1979), a method in which the -Asp-Pro- sequence is cleaved with formic acid (Biochem. Biophys. Res. Commun., Vol. 40, pp. 1173, 1970), a method in which -Asn-Gly- sequence is cleaved with hydroxylamine, a method in which the C-terminal end of trypsin is cleaved with BNPS-skatole or N-chlorosuccinimide, and the like. When methionine is not included in such an amino acid sequence of the peptide of interest, methionine is introduced at the end of the cleavage site region adjacent to the peptide of interest, and chemical

cleavage with cyanogen bromide at the cleavage site region can be carried out.

As an enzymatic cleavage method, it is required to design a cleavage site region that can be specifically recognized as a substrate by an enzyme used for the cleavage treatment. Examples of such methods include the cleavage of: the -X-Gly- sequence of the X-Gly or the Pro-X-Gly-Pro sequence with collagenase (Proc. Natl. Acad. Sci. U.S.A., Vol. 81, pp. 4692-4696, 1984); the C-terminal end of Lys of the -Asp-Asp-Asp-Lys- sequence (SEQ ID NO: 1) with enterokinase; the C-terminal end of Arg of -Ile-Glu-Gly-Arg- sequence (SEQ ID NO: 2) with blood coagulation factor Xa (Japanese Unexamined Patent Publication (Kokai) No. 61(1986)-135591); the C-terminal end of Arg of the -Gly-Pro-Arg- sequence with thrombin (Japanese Unexamined Patent Publication (Kokai) No. 62(1987)-135500); the C-terminal end of -Arg- with trypsin or clostripain; the C-terminal end of Arg or Lys with endoprotease Arg-C (Nature, Vol. 285, pp. 456-461, 1980); the C-terminal end of the Lys-Arg, Arg-Arg, or Pro-Arg sequence with Saccharomyces cereviceae Kex2 protease and derivatives thereof (Biochem. Biophys. Res. Commun., Vol. 144, pp. 807-814, 1987, Japanese Unexamined Patent Publication (Kokai) No. 1(1989)-199578); the C-terminal end of Lys with lysyl endopeptidase or endopeptidase Lys-C (Japanese Unexamined Patent Publication (Kokai) No. 61(1986)-275222); the C-terminal end of Asp or Glu with Staphylococcus aureus (S. aureus) V8 protease (Proc. Natl. Acad. Sci. U.S.A., Vol. 69, pp. 3506-3509, 1972); the C-terminal end of the -Phe-Arg- sequence with kallikrein (Japanese Unexamined Patent Publication (Kokai) No. 62(1987)-248489); Leu-Leu of the -Pro-Phe-His-Leu-Leu-Vla-Tyr- sequence (SEQ ID NO: 3) with renin (Japanese Unexamined Patent Publication (Kokai) No. 60(1985)-262595); the C-terminal end of the -Glu-Gly-Arg- sequence with urokinase (Japanese Unexamined Patent Publication (Kokai) No. 2(1990)-

100685); the C-terminal end of the Val-Asp-Asp-Asp-Asp-Lys sequence (SEQ ID NO: 4) with entero-peptidase (Biotechnology, Vol. 6, pp. 1204-1210, 1988); the C-terminal end of poly-Gly with lysostaphin (Japanese Unexamined Patent Publication (Kokaki) 1(1989)-160496); the C-terminal end of Lys-Arg, Arg-Arg, or Pro-Arg, etc. with Kluverromyces lactis) (Japanese Unexamined Patent Publication (Kokai) No. 1(1989)-124390), and the like.

In the Examples of the present invention, for example, an amino acid sequence (the Lys-Arg, Arg-Arg or Pro-Arg sequence) that can be recognized by Kex2 protease was introduced into the cleavage site region and then the peptide of interest was cleaved with the enzyme.

Depending on the substrate specificity of an enzyme used in the cleavage treatment and the amino acid sequence of the peptide of interest, therefore, it is preferred that one or more of methionine, tryptophan, proline, glycine, cysteine, arginine, lysine, aspartic acid, and glutamic acid is present in the amino acid sequence of the cleavage site region.

When modification is required to obtain a final peptide of interest (for example, an amidated peptide), a modification reaction (for example, an amidating modification reaction with an amidation enzyme) is carried out before or after excising said peptide of interest from the peptide of interest having a helper peptide added thereto (in this case the final peptide of interest is a production intermediate peptide).

Furthermore, efficient modification reaction is desired, a modification reaction (for example, an amidation modification reaction) is performed on the peptide of interest having a helper peptide added thereto before excising the peptide of interest to obtain the final peptide to which a helper peptide has been added, and then the cleavage site region in between the helper peptide and the final peptide of interest is cleaved to obtain the final peptide of interest.

If the peptide of interest having a helper peptide added thereto is highly expressed, the peptide of interest can be obtained at high purity and high yields, but in order to obtain larger amounts of the peptide of interest it can be produced by further adding a protective peptide and expressing it as has been conducted in the conventional fusion protein method. Thus, it is also possible to produce the peptide of interest at a high expression level within the host cell as a fusion protein further having a protective peptide added to the peptide of interest having a helper peptide added thereto (the protective peptide may be added to any of the N-terminal or C-terminal of the peptide of interest having a helper peptide added thereto).

The protective peptide for use in the production process of the present invention is not specifically limited and the conventionally used peptides can be used as appropriate with modifications. For example, in Japanese Unexamined Patent Publication (Kokai) No. 54(1979)-145289, fragments of the amino acid sequences from β -galactosidase derived from E. coli can be used as a protective peptide. The amino acid sequences of said enzyme are known to a person skilled in the art, and peptide fragments derived from β -galactosidase have been widely used as the protective peptide in the fusion protein method by persons skilled in the art. In the production processes of the present invention, peptide fragments that were obtained by appropriate modification of the amino acid sequences of β -galactosidase can be used as the protective peptide by taking into account the characteristics of the peptide of interest having a helper peptide added thereto. It is also possible to chemically synthesize a DNA base sequence encoding the amino acid sequence of the protective peptide.

For fusion proteins having a protective peptide, it is preferred to devise and obtain different isoelectric

points for each of the protective peptide, the peptide of interest having a helper peptide added thereto constituting said fusion protein, and said fusion protein, in order to enhance the fragment resolving ability during the chromatographic processes after the cleavage treatment reaction. The same is also true for the helper peptide and the peptide of interest.

When a protective peptide is added, as mentioned above, it is also necessary to provide a cleavage site region in between the peptide of interest having a helper peptide added thereto and the protective peptide, but it is possible to provide a cleavage site region having a preferable high cleavage efficiency as appropriate according to the above-mentioned strategy. However, when it is intended to obtain the peptide of interest through a fusion protein having the protective peptide to the peptide of interest having a helper peptide added thereto, a multi-step method of cleaving the fusion protein is required at each site since a plurality of cleavage site regions have been provided. In this case, the first cleavage treatment is carried out in the cleavage site region in between the peptide of interest having a helper peptide added thereto and the protective peptide, and then a cleavage treatment is carried out in the cleavage site region in between the helper peptide and the peptide of interest thereby to obtain the peptide of interest.

In order to confirm the wide applicability of the above production process, processes were examined, in the chemical or enzymatic cleavage of each cleavage site region and it was confirmed that any method of cleavage treatment can be carried out. Representative examples of the site-specific cleavage method of peptide at such cleavage site regions include:

(1) a method in which the absence of cysteine residues in the amino acid sequences of the protective peptide and the peptide of interest is utilized, and

cysteine is introduced in between the peptide of interest having a helper peptide added thereto and the protective peptide, which is then cyanized, subjected to an alkali treatment, and the fusion protein is specifically cleaved at the site;

(2) a method in which cleavage at each cleavage site region is carried out with the same enzyme, but by using different amino acid sequences at the enzyme recognition sites, the reaction condition for one cleavage site region is designed so as not to permit cleavage at another cleavage site region; and

(3) a method in which cleavage at each cleavage site region is carried out with the same enzyme, but by modifying amino acids in the cleavage site region (cleavage site region 2) present in between the helper peptide and the peptide of interest, the reaction condition for cleavage of the other cleavage site region (cleavage site region 1) present in between the peptide of interest having a helper peptide added thereto and the protective peptide is designed so as not to cause cleavage at cleavage site region 2, and after cleavage at cleavage site region 1, the peptide of interest having a helper peptide added thereto is purified, and then the modified amino acid is modified again so that cleavage site region 2 can be made possible to be cleaved with the above enzyme.

Host cells that can be used in the present invention are not specifically limited and the conventionally used prokaryotic cells or eukaryotic cells, for example microorganism cells such as E. coli, yeasts or animal cells that can suitably express, using an expression vector having a nucleotide sequence encoding, a peptide of interest having a helper peptide added thereto can be chosen as appropriate and used. Furthermore, other elements required for high expression such as a promoter, a terminator, and splice sites are also chosen from the conventionally used ones and used as appropriate.

In the production process of the peptide of interest of the present invention, the following describes a case wherein the peptide of interest is GLP-1(7-37) and GLP-1(7-36)NH₂.

5 The fusion protein (referred to hereinafter as GP97ompPR) encoded by the GLP-1(7-37) expression vector (referred to hereinafter as pGP97ompPR) is a fusion protein that has a peptide (referred to hereinafter as RHHGP[G]) having a helper peptide added thereto, said
10 helper peptide containing a basic peptide region in the N-terminal end of GLP-1(7-37), and that has an E. coli β -galactosidase derivative (β -gal97S) added to the N-terminal end of RHHGP[G] as a protective peptide. A
15 cleavage site region has been introduced in between the protective peptide and RHHGP[G] and between the helper peptide of RHHGP[G] and GLP-1(7-37). Each of the regions has amino acid sequences responsible for substrate
20 specificity so that one cleavage site region may be cleaved with an endogenous OmpT protease derived from E. coli, and the other cleavage site region may be cleaved with Kex2 protease (Japanese Patent No. 2643968, and Japanese Unexamined Patent Publication (Kokai) 10(1998)-229884, and the like).

25 For GP97ompPR, the isoelectric point of each of β -gal97S or RHHGP[G] and GP97ompPR has been designed to be different from each other, in order to enhance the fragment resolving ability in the chromatographic process after the cleavage treatment reaction. For example, in
30 Examples described below, the isoelectric point of GP97ompPR has been designed to be 5.95, that of β -gal97S to be 4.60, and that of RHHGP[G] to be 10.09.

35 Then, E. coli (W3110/pGP97ompPR) transformed with pGP97ompPR was cultured to express GP97ompPR. GP97ompPR was highly expressed as an insoluble protein in the cells and was accumulated in the inclusion bodies. The final cell density reached to 180 at OD660 nm.

After disrupting the cells, GP97ompPR was solubilized with urea, and the cleavage site region in between the protective peptide β -gal97S and the peptide of interest RHHGP[G] having a helper peptide added thereto in GP97ompPR was cleaved with the endogenous OmpT protease existing in the inclusion body. OmpT protease specifically cleaved said cleavage site region with a cleavage efficiency of 85%.

Next, in order to separate β -gal97S and RHHGP[G] and to remove urea, a cation exchange chromatography was carried out. Since the isoelectric points of non-cleaved GP97ompPR (pI = 5.95) and that of β -gal97S (pI = 4.60) were both in the acid side they do not adsorb to the column, and RHHGP[G] (pI = 10.09) was adsorbed and eluted. Through this one step of column treatment alone, RHHGP[G] at a purity of 99% was obtained. The fact that the first stage of column procedures during the production process provides RHHGP[G] at such a high purity and high yield is very useful from the viewpoint of industrial large-scale production.

The cleavage site region in between the helper peptide and the peptide of interest present in RHHGP[G] (1.0 g) was cleaved using Kex2 protease. In the reaction condition described in Examples below, the reaction proceeded at a cleavage efficiency of 95%. The recovery was 90%.

Subsequently, a reverse-phase chromatography was carried out to further purify GLP-1(7-37). The recovery of this process was 80%, the final yield of the overall processes was about 64% and 0.72 g of GLP-1(7-37) having a purity of 98% was obtained. Since the amount of the culture broth used for purification was about 0.36 liter, this means that about 2.0 g was obtained per liter of the culture broth. The recovery and the yield are both very high and thereby have proved the usefulness of the production method of the present invention that employs a

helper peptide. Thus, the production process of the present invention enables full realization of the production of the peptide of interest on an industrial scale.

5 Concerning the production of GLP-1(7-37) using the production process of the present invention, the yield at each step is shown in Table 2-B below.

 As can be seen from Table 2-B, it was demonstrated that the yield at each step is very high and the finally
10 recovery of 64% is very high.

 Furthermore, when the peptide of interest is GLP-1(7-36)NH₂, an amidation modification reaction is required since the peptide is an amidated peptide. The peptide can be obtained as follows:

15 RHHGP[G] obtained as mentioned above was subjected to an amidation modification reaction using an amidation enzyme (B. B. R. C., Vol. 150, pp. 1275-1281, 1988, EP299790A, and the like). Under the reaction condition in Examples described below, no aggregation or gelling of
20 RHHGP[G] as the enzyme substrate and the reaction product, amidated GLP-1(7-36)NH₂ (referred to hereinafter as RHHGP-1) having a helper peptide added thereto occurs, and RHHGP-1 could be produced at a high reaction rate of 98% (a recovery of 95%). These results demonstrated the
25 usefulness of the helper peptide in the amidation enzymatic reaction conducted with a substrate of RHHGP[G].

 After the amidation modification reaction, the cleavage site region in between the helper peptide and
30 the peptide of interest present in RHHGP-1 was cleaved using Kex2 protease. Under the reaction condition in Examples described below, the reaction proceeded at a cleavage efficiency of 95% (a recovery of 90%) or greater.

35 In order to further purify GLP-1(7-36)NH₂, a cation exchange chromatography and then a hydrophobic chromatography were carried out. The final yield of the

overall process was about 50% and 13.5 g of GLP-1(7-36)NH₂ with a purity of 98% was obtained. Since the amount of the culture broth used for purification was about 8 liters, this means that about 1.68 g was obtained per liter of the culture broth. The recovery and the yield are both very high and thereby it was demonstrated that the production method of the present invention that employs a helper peptide is very useful. Thus, the production process of the present invention enables full realization of the production of the peptide of interest on an industrial scale.

One object of the present invention on the production of GLP-1(7-36)NH₂ is to relieve aggregation and increase solubility at the time of reaction of modification enzymes such as an amidation enzyme described above through a peptide comprising GLP-1(7-37) having a helper peptide added thereto. In order to further investigate the usefulness of the present invention, RHHGP[G], RHHGP-1, GLP-1(7-37), and GLP-1(7-36)NH₂ were purified and the pH dependency of the solubility of each peptide was examined. As a result, GLP-1(7-37) was shown to have a low solubility in the range of pH 5.0 to pH 7.0 as expected. On the other hand, RHHGP[G] had a high solubility in the range of from pH 4.0 to about pH 6.0. The result confirmed that the substitution of RHHGP[G] having a helper peptide for GLP-1(7-37) as an enzyme substrate is useful since the amidation enzyme reaction is carried out in the weak acid region.

In the experiment that investigated the pH dependency of solubility of each peptide, RHHGP[G] and RHHGP-1 have shown a sudden reduction in solubility at about pH 6.0 and about pH 6.4, respectively. GLP-1(7-36)NH₂ formed precipitates or microcrystals with time. Thus, it is estimated that substances capable of increasing the solubility of RHHGP[G] and RHHGP-1 in the neutral to weak alkali region and substances capable of

increasing the solubility of the peptide of interest in the weak acid to weak alkali region would be very useful in the production process.

Thus, after an intensive study to search such substances, the inventors of the present invention have found that aggregation can be effectively prevented by adding to the reaction mixture a surfactant (for example, the addition of 0.1% Tween 80) in the case of RHHGP[G] and RHHGP-1, a surfactant (for example, the addition of 0.3% or greater of Tween 80) and/or a salt (for example, 100 mM or greater of NaCl) in the case of GLP-1(7-36)NH₂, and could prove the usefulness thereof by introducing it to the production method of the present invention.

For the production process of GLP-1(7-36)NH₂ using the production method of the present invention, the yield of each step obtained in the purification of GLP-1(7-36)NH₂ on a 10 g scale is collectively shown in Table 1 (20 liters of the producing organism W3110/pGP97ompPR was cultured and an 8 liter portion of the culture broth was used for the purification).

Table 1
Summary of production steps of GLP-1(7-36)NH₂

Steps	Amount of GLP-1(7-37) / GLP-1(7-36)NH ₂ (g)	Yield of Unit process (%)	Overall recovery (%)
Culture (corresponding to 8 L culture broth)	26.87	100	100
OmpT reaction	22.95	85.4	85.4
SP sepharose chromato.	20.22	98.8	76.2
Amidation enzyme reaction	20.70	100	77.0
Kex2 enzyme reaction	18.70	90.4	69.6
MacroPrep HS chromato.	16.78	93.7	62.4
Poros R2 chromato.	13.48	80.4	50.2

The amount of GLP-1(7-37) is shown for the process from the culturing to the amidation enzyme reaction, and the amount of GLP-1(7-36)NH₂ is shown for the process from the Kex2 step to the Poros R2 chromatography step. The amount of GLP-1(7-37) / GLP-1(7-36)NH₂ was calculated from the ratio of the peak area of HPLC to the number of

amino acids.

As is evident from Table 1, the yield of a unit process in each step is very high, and the overall yield was shown to be as very high as about 50%. Thus, it is clear that the process for producing peptides of the present invention can be applied to the production of GLP-1(7-36)NH₂ and that it can be scaled up to an industrial production level. Furthermore, since the yield of the unit process in the process of cleavage treatment reaction with OmpT protease and Kex2 protease is 85% and 90.4%, respectively, it was confirmed that each cleavage site region designed had amino acid sequences very suitable for the cleavage treatment reaction with the enzyme.

As hereinabove described, it was shown, as an example of the process for producing a GLP-1 derivative having an insulintropic activity, that the present invention can relieve the problems in production processes due to the intrinsic physicochemical properties of the peptide of interest. The problems on production due to the physicochemical properties of the GLP-1 derivatives represented by GLP-1(7-37) and GLP-1(7-36)NH₂ that were specifically described can be overcome using the production method according to the present invention, and, needless to say, the present invention is also useful for the production of GLP-1 derivatives.

The above-mentioned production of GLP-1 derivatives can be effected by a method using a fusion protein having a protective peptide added thereto. However, when the peptide of interest is obtained from said fusion protein through the peptide of interest having a helper peptide added thereto, multiple cleavage site regions are provided, and therefore a multi-step method of cleaving the fusion protein will be required.

Thus, the inventors have investigated on methods for chemically or enzymatically cleaving each cleavage site region, and have confirmed that it is possible by a

method other than the one that employs the cleavage with E. coli OmpT protease confirmed in particular in an Example described below. Representative examples of the site-specific cleavage method of peptide at such cleavage site regions include:

(1) a method in which the absence of cysteine residues in the amino acid sequences of the protective peptide and the peptide of interest is utilized, and cysteine is introduced at the C-terminal of the protective peptide, which is then cyanized, subjected to an alkali treatment to specifically cleave the fusion protein at said N-terminal of the cysteine;

(2) a method in which cleavage at each cleavage site region is carried out with Kex2 protease, but by using different amino acid sequences at the enzyme recognition sites, the reaction condition for one cleavage site region is designed so as not to permit cleavage at another cleavage site region; and

(3) a method in which cleavage at each cleavage site region is carried out with Kex2 protease, but by modifying amino acids in one cleavage site region (cleavage site region 2), the reaction condition for cleavage of the other cleavage site region (cleavage site region 1) is designed so as not to cause cleavage at the former cleavage site (cleavage site region 2), and after cleavage at the latter cleavage site region (cleavage site region 1), the peptide comprising a helper peptide and the peptide of interest is purified, and then the modified amino acid is modified again so that the former cleavage site region (cleavage site region 2) can be made possible to be cleaved with Kex2 protease.

EXAMPLES

With a GLP-1 derivative as the peptide of interest, the present invention will now be explained in further detail with reference to the following Examples.

As a production process when the peptide of interest is GLP-1(7-37), as described above, the peptide can be

produced by expressing a fusion protein comprising the protective peptide and GLP-1(7-37) in a conventional method, and then by excising GLP-1(7-37) directly from said protein. However, this method had problems on the purification process in which the gelling or aggregation of GLP-1(7-37) occurred during purification due to its physicochemical properties, which resulted in such problems as extreme reduction in recovery and incapacitation of regeneration of the resin. This drawback could be circumvented by changing the physicochemical properties of GLP-1(7-37) by adding a helper peptide thereto. The method for producing said peptide is now explained more specifically below.

Example 1. Construction of plasmid

An expression plasmid pGP97ompPR that encodes a fusion protein (GP97ompPR) designed for the production of GLP-1(7-37) was prepared through the 4 steps shown below. The restriction enzyme treatment, the ligation reaction, the phosphorylation of the 5'-end, and PCR conditions were carried out according to conventional methods.

(1) Step 1 Construction of pG117S4HR6GLP-1

In order to design GP97ompPR that can be cleaved with E. coli OmpT protease, R6 synthetic DNA (see Figure 6) encoding the amino acid sequence R6 (see Figure 2) having the Arg-Arg sequence, a recognition sequence for OmpT protease, was inserted into a StuI site of pG117S4HGP (see Japanese Unexamined Patent Publication (Kokai) No. 9(1997)-296000) to construct pG117S4HR6GLP-1 (Figure 2).

(2) Step 2 Construction of pGP117S4HomprHKKR

In order to further enhance the efficiency of cleavage by E. coli OmpT protease, the sequence of the R6 portion was changed. A 3.2 kb fragment (fragment A) obtained by cleaving pG117S4HR6GLP-1 with Nsi I and Hind III was ligated to a 0.2 kb fragment (fragment B) obtained by cleaving PG117S4HR6GLP-1 with BamH I and Hind III and L1 synthetic DNA (see Figure 6) encoding a

portion of the amino acid sequence L1 (see Figure 3) having the Arg-Arg sequence, a recognition sequence for OmpT protease, to construct pGP117S4HomprHKKR (Figure 3).

(3) Step 3 Construction of pGP117S4HomprHPR

5 In order to make the E. coli OmpT protease recognition sequence and the Kex2 protease recognition sequence different from each other in the cleavage site region, Lys-Arg in the Kex2 protease recognition sequence was replaced with Pro-Arg. P1 primer and P2 primer (see 10 Figure 6) were synthesized, which were subjected to PCR using pGP117S4HomprHKKR as the template to construct a 0.1 kb DNA fragment. After treating the thus obtained DNA fragment with Bgl II and Sph I, it was ligated to a 3.2 15 kb fragment (fragment C) obtained by cleaving pGP117S4HomprHKKR with Bgl II and Hind III and a 0.2 kb fragment (fragment D) obtained by cleaving pGP117S4HomprHKKR with Sph I and Hind III to construct pGP117S4HomprHPR (Figure 4).

(4) Step 4 Construction of pGP97ompPR (Figure 5)

20 In order to further reduce the size of the protective peptide portion, pGP97ompPR was constructed. P3 and P4 primers (see Figure 6) were synthesized, which were subjected to PCR using pGP117S4HomprHPR as the template to construct a DNA fragment. After treating the 25 thus obtained DNA fragment with Pvu II and Nsi I, it was ligated to a 3.2 kb fragment obtained by cleaving pGP117S4HomprHPR with Pvu II and Nsi I to construct pGP97ompPR.

The amino acid sequence of the fusion protein 30 (GP97ompPR) encoded by the thus constructed plasmid pGP97ompPR is shown in Figure 7, and the DNA nucleotide sequence encoding said amino acid sequence is shown in Figure 8.

Example 2. Expression of fusion protein (GP97ompPR)

35 E. coli strain W3110 having pGP97ompPR was cultured in a culture medium (20 L, pH 7.0) containing 4 g/l K_2HPO_4 , 4 g/l KH_2PO_4 , 2.7 g/l Na_2HPO_4 , 0.2 g/l NH_4Cl , 1.2

g/l $(\text{NH}_4)_2\text{SO}_4$, 4 g/l yeast extract, 2 g/l $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 40 mg/l $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$, 40 mg/l $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 10 mg/l $\text{MnSO}_4 \cdot n\text{H}_2\text{O}$, 10 mg/l $\text{AlCl}_3 \cdot 6\text{H}_2\text{O}$, 4 mg/l $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$, 2 mg/l $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$, 2 mg/l $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 1 mg/l $\text{CuCl}_2 \cdot 2\text{H}_2\text{O}$, 0.5 mg/l H_3BO_4 , and 10 mg/l tetracycline in a 30-liter jar fermenter at a temperature of 32°C for 12 hours and thereafter at 37°C for 24 hours while adding glucose. The pH of the medium was controlled at pH 7.0 by adding a 28% ammonium solution. Figure 9 is the result of changes in cell density (OD660), and the expression of the fusion protein (GP97ompPR) at the time of sampling that were analyzed with 16% SDS-PAGE. GP97ompPR was expressed as the inclusion body and accounted for 30% or more of the total cellular protein at the end of culturing.

After culturing, the culture broth was homogenized at 500 Kg/cm² using a Manton-Gaulin homogenizer (15M-8TA), and then was centrifuged to collect the precipitate fraction (inclusion body). Then, in order to wash the obtained precipitate, an equal amount of deionized water was added to the culture broth. After suspension, centrifugation was repeated to collect the precipitate. The washing process was repeated again and finally the obtained precipitate was suspended in a suitable amount of deionized water.

Example 3. Processing of GP97ompPR with E. coli OmpT protease

The obtained suspension of the inclusion body was diluted to give an OD660 value of 1000. From the liquid a 1000 ml portion was taken, to which 250 ml of 1M Tris-HCl for which pH has not been adjusted, 10 ml of 0.5 M EDTA (pH 8.0), and 1200 g of powdered urea was added, and then deionized water was added thereto to give a final volume of 5000 ml. Then HCl was used to adjust pH at 7.5 and the liquid was heated to 37 °C for 2 hours. This procedure initialed the action of E. coli OmpT protease present in the inclusion body, and GP97ompPR was cleaved

and RHHGP[G] was released. Figure 10 is the result of the RHHGP[G] that was excised from GP97ompPR and then was analyzed with reverse phase HPLC. The analysis used a YMC PROTEIN-PR column, a 10% acetonitrile solution containing 0.1% trifluoroacetic acid as solution A and a 70% acetonitrile solution containing 0.095% trifluoroacetic acid as solution B, with a flow rate of 1 ml/min and a linear gradient of solution B from 44% to 70% in 13 minutes. This procedure cleaved 85% of GP97ompPR and at the end of the reaction a peak corresponding to RHHGP[G] was obtained (Figure 21 A).

The excision of GLP-1(7-37) having a helper peptide added thereto from the fusion protein by the cleavage treatment with *E. coli* OmpT protease was not limited to the fusion protein derived from pGP97ompPR, and was also possible for fusion proteins derived from pG117S4HR6GLP-1, pGP117S4HomprHHR and pGP117S4HomprHPR constructed in Example 1. The amino acid sequences of these fusion proteins derived from plasmids are shown in Figures 11, 12, and 13.

Example 4. Purification of RHHGP[G]

After the *E. coli* OmpT protease reaction, urea and Tween 80 were added to a concentration of 7M and 0.1%, respectively, and pH was adjusted to 8.0 with NaOH. The mixture was then centrifuged to obtain a supernatant. A column charged with SP-Sepharose BigBeads (Amersham Pharmacia Biotechnology) was equilibrated with 100 mM Tris HCl, pH 8.0, and then 20 mM Tris HCl, pH 8.0 / 5 M urea / 0.1% Tween 80. After the above supernatant was added to the equilibrated column, the column was washed in the same equilibration solution, and then was washed with 0.2 M NaCl / 20 mM Tris HCl, pH 8.0 / 0.1% Tween 80 and eluted with 0.5 M NaCl / 20 mM Tris HCl, pH 8.0 / 0.1% Tween 80 (Figure 14).

The purity of RHHGP[G] in the eluate was as high as 98%. The reason why such a high purity peptide could be obtained by a simple procedure of the addition of a

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Table 2
Comparison of GLP-1(7-37) production process

A

Process	Purity (%)	Yield of unit process (%)	Overall recovery (%)
Kex2 enzyme reaction	15	-	100
Acid precipitation treatment	-	68	68
Filtration	75	88	60
Cation exchange chromatography	95	95	57
Reverse phase chromatography	99	72	41

5

B

Process	Purity (%)	Yield of unit process (%)	Overall recovery (%)
OmpT reaction	24	-	100
Filtration	24	90	90
Cation exchange chromatography	99	99	89
Kex2 enzyme reaction	96	90	80
Reverse phase chromatography	98	80	64

10 A is based on a method of excising GLP-1(7-37) directly from a fusion protein comprising a protective peptide and the peptide of interest. B is based on a method of excising GLP-1(7-37) from a fusion protein having a protective peptide further added to the peptide of interest having a helper peptide added thereto.

15 By using RHHGP[G] as an intermediate, GLP-1(7-37) having a purity of 99% was obtained at ease and at a high yield. Since HPLC is not used in the purification of the present invention, it is, needless to say, easy to scale up to an industrial scale.

20 The following is an example wherein a peptide of interest requires modification. Since GLP-1(7-36)NH₂ is an amidated peptide, an amidation modification reaction is required.

25 Example 6. An amidation modification reaction of GLP-1(7-37) having a helper peptide added thereto

RHHGP[G] obtained in Example 4 was converted to RHHGP-1 using an amidation enzyme. In order to determine the reaction condition for the case wherein RHHGP[G] was

used as a substrate, optimization was carried out for pH, temperature, the concentration of copper sulfate, catalase concentration, substrate concentration, L-ascorbic acid concentration, and the concentration of the amidation enzyme in a reaction volume of 0.5 ml.

Separation of RHHGP[G] and RHHGP-1 and analysis thereof were carried out using an ion exchange HPLC column (Poros S/H, Perceptive Biosystems) in the presence of 30 mM Britton-Robinson buffer (referred to hereinafter as the BR buffer) excluding barbital at a pH gradient elution (6.0 to 9.0).

The optimum pH of the reaction condition was 5.0 to 5.5 (Figure 16). The optimum reaction condition was 10 mM sodium acetate, pH 5.0, 5.0 μ M copper sulfate, 0.5 g/l L-ascorbic acid, 1 μ M/ml catalase, 5.0 mg/ml RHHGP[G], a temperature of 32 °C, and 1500 units/ml amidation enzyme. To this condition was added Tween 80 (0.1%) that was found to have an aggregation suppression effect in Example 11 below, 5 liters of the RHHGP[G] solution was reacted in the above condition, and the reaction was stopped by adding EDTA. As a result of the reaction under the present condition, RHHGP[G] was converted with RHHGP-1 with a reaction rate of 98% or greater in one hour (Figure 17).

Example 7. Excision of GLP-1(7-36)NH₂ from RHHGP-1 with Kex2 protease

The processing reaction with Kex2 protease shows a pH dependency and activity change depending on the sequence of the portion that serves as the substrate (EP794255A). Accordingly, the optimization of pH, calcium chloride concentration and the amount of the enzyme added was carried out in a reaction volume of 0.5 ml. In the case of RHHGP-1, the reaction was shown to reach the maximum at pH 8.0 (Figure 18). The optimum reaction condition when RHHGP-1 was used as the substrate was set at 10 mM Tris-HCl, pH 8.0, 1 mM calcium chloride,

8,000 units/ml Kex2 protease and a reaction temperature of 30°C to 32°C. From the results in Example 11 below, aggregation could be avoided by setting the NaCl concentration in the reaction mixture at 0.1 M or greater and by further adding Tween 80 to a concentration of 0.1%.

By reacting the sample solution after the amidation reaction in Example 6 at 30°C under the present condition for 2 hours, a reaction rate of 95% or greater was obtained (Figure 21C). During the reaction, no precipitate formation of GLP-1(7-36)NH₂ was observed.

Example 8. Purification of GLP-1(7-36)NH₂

In order to remove impurities at minute amounts, a pH gradient elution using a cation exchange resin (MacroPrep High-S, BioRad) was used to separate GLP-1(7-36)NH₂ therefrom. The column was equilibrated with 20 mM BR buffer, pH 4.5 / 20 mM NaCl / 0.3% Tween 80. The composition of the sample solution was set at 0.3 M NaCl / 0.3% Tween 80, pH 4.5. The sample solution was added to the column, which was washed in the equilibration solution. Using the equilibration solution (solution A) and the elution solution (solution B; pH 7.0 with the same composition as the equilibration solution), GLP-1(7-36)NH₂ was eluted in a linear gradient from 50% solution B to 100% solution B (Figure 19) to make the proportion of the impurities less than 0.5% (Figure 20). In this process, most of the reagents added up to Example 7, unreacted products, and trace amounts of impurities were removed, and GLP-1(7-36)NH₂ with a purity of 98% or greater was obtained (Figure 21D). The pooled solution had a pH of 4.5 and was stored at 4 °C.

Example 9. Final purification of GLP-1(7-36)NH₂

In the above Example 8, GLP-1(7-36)NH₂ with a purity of 98% or greater was obtained. When used as a pharmaceutical drug, however, not only the purity of the peptide of interest is important, but the contamination of non-peptide endotoxin must be avoided. Accordingly,

in attempts to remove endotoxin etc., a preparative reverse phase HPLC column that is often used for the final purification of peptide drugs was used. But there were times when the aggregation and/or gelling of GLP-1(7-36)NH₂ occurred in the column. It was expected that the tendency of GLP-1(7-36)NH₂ to aggregate easily provides a major risk factor in scaling up.

On the other hand, although the hydrophobic chromatographic resin adsorbs substances utilizing the hydrophobicity thereof as with the reverse phase chromatographic resin, it is generally low in the density of functional groups and has an adsorption volume of 5 to 15 mg/ml resin. However, there are many kinds of carriers and many kinds of functional groups, and therefore it is possible to choose peptides that give a high recovery rate even when they have a tendency to easily aggregate like GLP-1(7-36)NH₂. After investigating various functional hydrophobic chromatographic resins, we have found that resins comprising hydrophilic carriers having butyl groups, isobutyl groups, hexyl groups or phenyl groups resins or polystyrene resins represented by Poros R2 are suitable. One example of such a resin, Poros R2 (Perceptive Systems) is shown below.

A maximum adsorption volume of the resin for GLP-1(7-36)NH₂ is about 12 mg/ml resin, which is higher than the other hydrophobic chromatographic resins, and which results in a higher concentration of GLP-1(7-36)NH₂ during elution, suggesting that the resin is suitable for lyophilization.

A 800 ml column was equilibrated with 10 mM ammonium acetate, pH 4.5, to which was added the sample solution of Example 8. After washing with the equilibration solution, the column was further washed with 0.2% acetic acid, and was eluted with 0.2% acetic acid / 40% acetonitrile. The recovery of GLP-1(7-36)NH₂ was 80% and the purity was 98% (Figure 21E). The product only

contains volatile acids at a low concentration and therefore could be easily lyophilized after removal of acetonitrile. After reconstituting the lyophilized product, endotoxin was measured by the gelling method (Limulus ES-II test, Wako Pure Chemicals Co., Ltd.) and was found to be below the detection limit (0.03 μ /mg or lower). The fact that the column procedure described in the above method permits the purification of high yield and high purity GLP-1(7-36)NH₂ and enables elution by a solvent that can be lyophilized is, needless to say, industrially very useful.

Example 10. Alleviation of aggregation using a helper peptide

One object of the production method of the present invention that employs a helper peptide is to alleviate the aggregation property that is a characteristics derived from the physicochemical properties of the peptide of interest, which has been a problem in the conventional production method, and therefore it is necessary to investigate the presence of the alleviation. In the present Example, therefore, it was investigated whether the aggregation property of a peptide comprising a helper peptide and GLP-1(7-37) and a peptide comprising a helper peptide and GLP-1(7-36)NH₂ has been improved compared to that of GLP-1(7-37) and GLP-1(7-36)NH₂.

First, RHHGP[G] was purified and the improvement of the aggregation property compared to that of GLP-1(7-37) was investigated and at the same time substances that suppress aggregation were researched. Each of peptide samples, i.e. a sample prepared by purifying with SP-sepharose BigBeads chromatography for RHHGP[G], a sample prepared by amidating with purified RHHGP[G] for RHHGP-1, a sample prepared by cleaving RHHGP[G] with Kex2 protease for GLP-1(7-37), and a sample prepared by cleaving RHHGP-1 with Kex2 protease for GLP-1(7-36)NH₂, was purified to a purity of 98% by eluting with an acetonitrile concentration gradient using the Poros R2 column, and

then lyophilized to prepare each sample.

Since the aggregating property is considered to be associated with the solubility of each peptide, the pH dependency of the solubility of each peptide was investigated. The results are shown in Figure 22 and 23. It can be seen that GLP-1(7-37) is low in solubility in the range of pH 5.5 to pH 6.5, i.e., from the weak acid to the neutral condition which is optimum pH for the amidation enzyme reaction condition, indicating that it is inappropriate as a production intermediate.

On the other hand, although RHHGP[G] and RHHGP-1 start to show decreased solubility at about pH 6.2, they retain adequate solubility at least up to pH 5 or pH 6, and it was confirmed that they could be adequately efficiently reacted even under the amidation enzyme reaction condition.

Example 11. Screening of substances having aggregation suppression

In the establishment of the production method of GLP-1(7-36)NH₂ on an industrial level using the production method of the present invention that employs a helper peptide, a substance that increases the solubility of RHHGP[G] and RHHGP-1 in the neutral to the weak alkali region and that maintain the solubility of GLP-1(7-36)NH₂ in the weak acid to the weak alkali region, if present, would be more preferred (GLP-1(7-36)NH₂ lags behind GLP-1(7-37) in the study shown in Figure 22, but it was found that it forms precipitates or microcrystals with time in the broad range of pH 5.3 to pH 8.0).

As the substances that are added to the solution so as to be able to maintain the solubility of each peptide, possible candidates include surfactants, sugars, salts, organic solvents and the like. Therefore, Tween 80 and Triton X100 as a surfactant, glucose, mannitol, and sucrose as a sugar, NaCl as a salt, and ethanol, glycerol, and DMSO as an organic solvent were tested for their ability of suppressing aggregation.

Ten mg/ml aqueous solutions of RHHGP[G], RHHGP-1, and GLP-1(7-36)NH₂ were prepared. To plastic tubes containing 0.1 ml of 300 mM BR buffer, pH 7.9, and 0.1 ml of 10-fold concentrated test sample solutions, 0.8 ml of each peptide solution was added, and pH was adjusted to levels that can easily cause aggregation, such as pH 7.5 to 8.5 for RHHGP[G], pH 8.0 for RHHGP-1, and pH 6.5 for GLP-1(7-36)NH₂, and then turbidity (absorbance at 660 nm) with time was monitored. Among the results obtained, the suppressive effects on aggregation by Tween 80, NaCl, and temperature are shown in Figure 23 and Figure 24.

It was found that precipitate formation was strongly suppressed with 0.1% Tween 80 in RHHGP[G] and RHHGP-1 (Figure 23A), but in GLP-1(7-36)NH₂ aggregation was suppressed by Tween 80 at 0.3% or higher (Figure 23B), NaCl at 100 mM or higher (Figure 24C), and/or at low temperature (Figure 24D).

From the above results, it was demonstrated that with regard to the pH condition in the actual production system, the addition of a salt and a surfactant are useful for suppressing the aggregation of the peptide of interest when the method for producing peptides of the present invention is used, and was indicated that the peptide of interest can be produced at high purity and high yields.

Example 12. Methods of cleaving in the cleavage site region

Methods of cleaving used when cleaving is carried out at cleavage site regions were investigated. Thus, when the cleavage method for each of the case (1) cleavage site region 1: cyanization / alkalization, cleavage site region 2: Kex2 protease; (2) cleavage site region 1: Kex2 protease, cleavage site region 2: Kex2 protease; and (3) cleavage site region 1: DTNB (5,5'-dithiobis-(2-nitrobenzoic acid)) addition / Kex2 protease, cleavage site region 2: reduction / Kex2 protease was investigated using the peptide of interest

as GLP-1(7-37) and GLP-1(7-36)NH₂, it was found that cleavage by a multi-step cleavage method can be carried out by a chemical or enzymatic treatment when a fusion protein comprising a protective peptide is used in the production method of the present invention.

Results for each method are shown below. In order to enhance hydrophilicity of the polypeptide comprising a helper peptide and GLP-1(7-37) formed after cleavage and thereby to improve the solubility at neutral pH, 4 contiguous histidine sequences were introduced in all helper peptides.

A. A method of producing GLP-1(7-37) through specific cleavage at the cysteine residue using method (1)

This method chemically cleaves a cysteine residue in one cleavage site region (cleavage site region 1) when the peptide of interest does not contain cysteine. For example, it was confirmed that after the fusion protein was expressed and obtained and a cysteine residue was cyanized with CADP (1-cyano-4-dimethylamino-pyridinium tetrafluoroborate), it could be specifically cleaved at the N-terminal side of cysteine of the cleavage site region by an alkali (NaOH) treatment.

Thus, PGGRPSRHKR (SEQ ID NO: 6) was selected as an amino acid sequence in cleavage site region 1 adjacent to the amino acid sequence of GCHHHH (SEQ ID NO: 5) as a helper peptide, and was introduced into a fusion protein. Said fusion protein was dissolved at 30 mg/ml in 50 mM Tris-HCl, pH 8.2, 5 M urea, and 10 mM DTT (dithiothreitol), and incubated in a 30°C incubator for 30 minutes to completely reduce cysteine. This was subjected to a gel-filtration column (manufactured by Pharmacia, PD10 column) that had been equilibrated with 10 mM Tris-HCl, pH 8.2, and 5 M urea to remove DTT.

In order to cyanize cysteine, acetic acid was added to a final concentration of 0.1 M, and CADP at 4-fold mole greater amounts than cysteine was added thereto and

was reacted at 30°C for 1 hour. Cyanization reaction was confirmed by determining the residual SH groups with DTNB.

5 The above fusion protein was specifically cleaved at the cyanized cysteine site by removing an excess of reagents with a PD10 column equilibrated with 10 mM acetic acid and 5 M urea, adding NaOH to a final concentration of 50 mM, and then leaving it at room temperature for 30 minutes. The rate of cleavage was
10 about 50 to 70%.

The other cleavage site region (cleavage site region 2) was subjected to a cleavage treatment in a similar manner to Example 7.

15 B. Cleavage of a cleavage site region with Kex2 protease using method (2)

It was designed that while each cleavage site region has a Kex2 protease cleavage site region, the amino acid sequence of one cleavage site region (cleavage site region 2) is hardly cleaved under the reaction condition
20 for the cleavage of the other cleavage site region (cleavage site region 1).

It is known that in the optimization of a cleavage recognition sequence in the cleavage site region of Kex2 protease, the charge of the amino acid residue at the P4 subsite, in addition to the P1 and P2 subsites, greatly influences the activity of the enzyme and that the fusion protein is not cleaved at all under a certain condition especially when an acidic amino acid is present at the P4 subsite (Japanese Unexamined Patent Publication (Kokai)
25 9(1997)-296000). By utilizing this, for example, by introducing aspartic acid (D) into the P4 subsite as the amino acid sequence SDHKR (SEQ ID NO: 8) of cleavage site region 2 adjacent to an amino acid sequence comprising HRHKRSHHHH (SEQ ID NO: 7) as a helper peptide, 90% or
30 greater was cleaved with Kex2 protease in the cleavage of cleavage site region 1 in the fusion protein but cleavage site region 2 was protected from the cleavage. The
35

result revealed that cleavage site region 1 can be specifically cleaved by introducing aspartic acid into the P4 subsite.

5 In an ion exchange chromatography and a column chromatography (for example, Cellulofine C-200 column chromatography) having a gel filtration ability that were carried out in order to isolate the obtained GLP-1(7-37) having a helper peptide added thereto, the desired GLP-1(7-37) having a helper peptide added thereto was
10 specifically adsorbed. Some of the unreacted fusion protein also adsorbed but they were readily separated by a salt concentration gradient. The recovery was 94%. The chromatography can also be applied to GLP-1(7-36)NH₂ having another helper peptide added thereto.

15 Subsequently, after an amidation modification reaction, Kex2 protease cleavage treatment was carried out at cleavage site region 2 in order to excise GLP-1(7-36)NH₂ from GLP-1(7-36)NH₂ having a helper peptide added thereto. It was found that under the first
20 cleavage condition which contained urea (denaturant) and which was alkaline, Kex2 protease did not cleave cleavage site region 2, but in the absence of urea cleavage site region 2 could be recognized by choosing an appropriate pH. It was shown that the optimum pH was 6.5 to 7.3 and
25 thus cleavage was not easy at pH 8.2 which is a cleavage reaction condition in cleavage site region 1.

This is because the above GLP-1(7-36)NH₂ having a helper peptide added thereto is different from the fusion protein having a protective peptide further added thereto
30 and is soluble in a wide pH range even in the absence of urea. Thus, Kex2 protease was allowed to react and the peptide was separated and determined with a reverse phase HPLC with the cleavage of 98% or greater being defined as complete. Since the system does not contain urea, the
35 activity loss of Kex2 protease hardly occurs. Thus, it has an advantage that the amount of Kex2 protease required is extremely small, with a molar ratio to the

substrate being 1:20000 to 1:40000.

As mentioned above, it was demonstrated that GLP-1(7-37) and GLP-1(7-36)NH₂ could be produced by using the same enzyme in cleavage treatment of each cleavage site region.

C. Cleavage method utilizing a specific modification of cysteine using method (3)

This method is almost similar to method (2) and, when the peptide of interest does not contain cysteine residues, it modifies the cysteine residue introduced into the P4 subsite of one cleavage site region (cleavage site region 2), i.e. it protects the cleavage site region 2 from cleavage at the time of Kex2 protease cleavage reaction at the other cleavage site region (cleavage site region 1) by treating the side chain of cysteine with DTNB (dithionitriobenzoic acid), carries out reduction after a peptide comprising GLP-1(7-37) having a helper peptide added thereto was obtained, to thereby cleave cleavage site region 2 with Kex2 protease.

Representative examples of such modification reactions include sulfonation and asymmetric disulfidization with DTNB, but are not limited to these reactions as long as the method gives a negative charge to the cysteine side chain. For example, the amino acid sequence of cleavage site region 2 adjacent to the amino acid sequence comprising HRHKRSHHHH (SEQ ID NO: 7) as a helper peptide is introduced into a fusion protein as SCHKR (SEQ ID NO: 24).

The fusion protein designed as above was expressed, the fusion protein obtained was subjected to a DTNB treatment, and cysteine was made an asymmetric disulfide. After confirming the complete modification of cysteine, cleavage treatment reaction with Kex2 protease was carried out, and then it was confirmed that a peptide comprising GLP-1(7-37) having a helper peptide added thereto in a quantitative manner could be obtained. Thus, by changing the P4 subsite of the amino acid

sequence recognition site of Kex2 protease at cleavage
site region 2 to cysteine, and by introducing a negative
charge in a side chain-specific manner, cleavage site
region 2 was protected from cleavage at the time of
5 cleavage with Kex2 protease at cleavage site region 1.

Then, purification and an amidation reaction was
carried out as in the above B, DTT was added to reduce
GLP-1(7-36)NH₂ having a helper peptide added thereto,
hydrophobic column chromatography was carried out to
10 purify to a purity of 98%, and then the product was
lyophilized. When the product was dissolved at 5 mg/ml
in 20 mM BisTris, pH 7.0, and 2 mM calcium chloride, 1000
units/ml of Kex2 protease was added thereto, and the
mixture was reacted at 30°C, GLP-1(7-36)NH₂ having a
15 helper peptide added thereto was specifically cleaved to
give GLP-1(7-36)NH₂.

Although cleavage site region 2 was in a reduced
state in this example, it is possible, needless to say,
to modify it to have a positive charge and thereby to
20 change its reactivity to Kex2 protease.

Industrial Applicability

In accordance with the present invention, a method
for producing biologically active peptides efficiently
and at low cost on an industrial scale is provided.
25 Specifically, it was demonstrated, as described in
Examples of the present invention, that GLP-1 derivatives
for which industrial production has been difficult can be
produced at high purity and high yields. The production
method of the present invention can be applied to the
30 production of biologically active peptides other than
GLP-1 derivatives and thus are industrially extremely
useful.

CLAIM

1. A process for producing a peptide having a desired biological activity, comprising the steps of:

(1) culturing cells transformed with an expression vector having the nucleotide sequence encoding a peptide of interest that has a helper peptide added thereto, or a fusion protein that has a protective peptide further added to the peptide of interest that has a helper peptide added thereto; and then harvesting said peptide of interest that has a helper peptide added thereto or said fusion protein from said culture;

(2) in the case wherein a fusion protein is obtained in step (1), cleaving off from said fusion protein the peptide of interest that has a helper peptide added thereto and the protective peptide, and purifying the peptide of interest that has a helper peptide added thereto as desired;

(3) in the case wherein modification is required for the peptide of interest, subjecting the peptide of interest that has a helper peptide added thereto obtained in step (1) or step (2) to a modification reaction;

(4) cleaving off from the peptide of interest that has a helper peptide added thereto obtained in step (1), step (2) or step (3), the helper peptide and the peptide of interest, and purifying the peptide of interest as desired; and

(5) purifying the peptide of interest obtained in step (4).

2. The process according to claim 1, wherein said helper peptide has 5 to 50 amino acid residues.

3. The process according to claim 1 or 2, wherein said peptide of interest having a helper peptide added thereto has an isoelectric point of 8 to 12.

4. The process according to any of claims 1 to 3, wherein said peptide of interest has not more than 200 amino acid residues.

5. The process according to any of claims 1 to 4, wherein said protective peptide has 30 to 200 amino acid residues.

5 6. The process according to any of claims 1 to 5, wherein an ion exchange resin is used in the purification process.

7. The process according to claim 6, wherein said ion exchange resin is a cation exchange resin.

10 8. The process according to any of claims 1 to 5, wherein a reverse phase chromatography or a hydrophobic chromatography is used in the purification process.

15 9. The process according to any of claims 1 to 8, wherein a surfactant and/or a salt are added in at least one of steps (1) to (5) to maintain the solubility of the peptide of interest.

10. The process according to any of claims 1 to 9, wherein the host cell is a prokaryotic cell or a eukaryotic cell.

20 11. The process according to claim 10, wherein the host cell is Escherichia coli.

12. The process according to any of claims 1 to 11, wherein the isoelectric point of the peptide of interest having a helper peptide added thereto is 8 to 12.

25 13. The process according to any of claims 1 to 11, wherein the peptide of interest is an amidated peptide.

14. The process according to any of claims 1 to 11, wherein the peptide of interest is a GLP-1 derivative having an insulinotropic activity.

30 15. The process according to claim 14, wherein the GLP-1 derivative having an insulinotropic activity that has a helper peptide added thereto has an isoelectric point of 8 to 12.

35 16. The process according to claim 14 or 15, wherein the GLP-1 derivative having an insulinotropic activity has an isoelectric point of 4.5 to 9.0.

17. The process according to claim 14 or 15, wherein the GLP-1 derivative having an insulinotropic

activity has an isoelectric point of 5.5 to 7.5.

18. The process according to any of claims 12 to 17, wherein an ion exchange resin is used in the purification process.

5 19. The process according to claim 18, wherein said ion exchange resin is a cation exchange resin.

20. The process according to any of claims 12 to 17, wherein a reverse phase chromatography or a hydrophobic chromatography is used in the purification process.

21. The process according to any of claims 12 to 17, wherein a surfactant and/or a salt is added to maintain the solubility of the peptide of interest.

22. The process according to any of claims 14 to 21, wherein the purity of the GLP-1 derivative obtained having an insulinotropic activity is 98% or greater.

23. The process according to any of claims 1 to 22, wherein the content of endotoxin in the final purified product is not greater than 0.03 units/mg.

20 24. A pharmaceutical composition for treatment of diabetes mellitus comprising as an active ingredient a GLP-1 derivative having an insulinotropic activity, obtained from the process according to any of claims 14 to 23.

25 25. An expression vector comprising a nucleotide sequence encoding a peptide of interest that has a helper peptide added thereto, or a fusion protein that has a protective peptide further added to the peptide of interest that has a helper peptide added thereto.

30 26. A prokaryotic or a eukaryotic cell transformed with an expression vector comprising a nucleotide sequence encoding a peptide of interest that has a helper peptide added thereto, or a fusion protein that has a protective peptide further added to the peptide of interest that has a helper peptide added thereto.

35 27. The cell according to claim 26, wherein the host cell is Escherichia coli.

ABSTRACT

In the production of peptides having a desired biological activity using genetic engineering technology, it is characterized that said peptide of interest is expressed with addition of a helper peptide to said peptide of interest. This results in the enhancement in the purification efficiency and the yield of the peptide of interest through the prevention of aggregation during the recovery and/or purification process by adjusting isoelectric points, the enhancement of recovery in ion exchange chromatography, the enhancement of solubility of a fusion protein during the enzyme reaction for release the peptide of interest by enzymatic cleavage when the peptide of interest is expressed as a fusion protein with another peptide, the enhancement of solubility of said peptide during the enzyme reaction when the enzymatic modification of the peptide of interest is required, and the like.

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Fig. 1

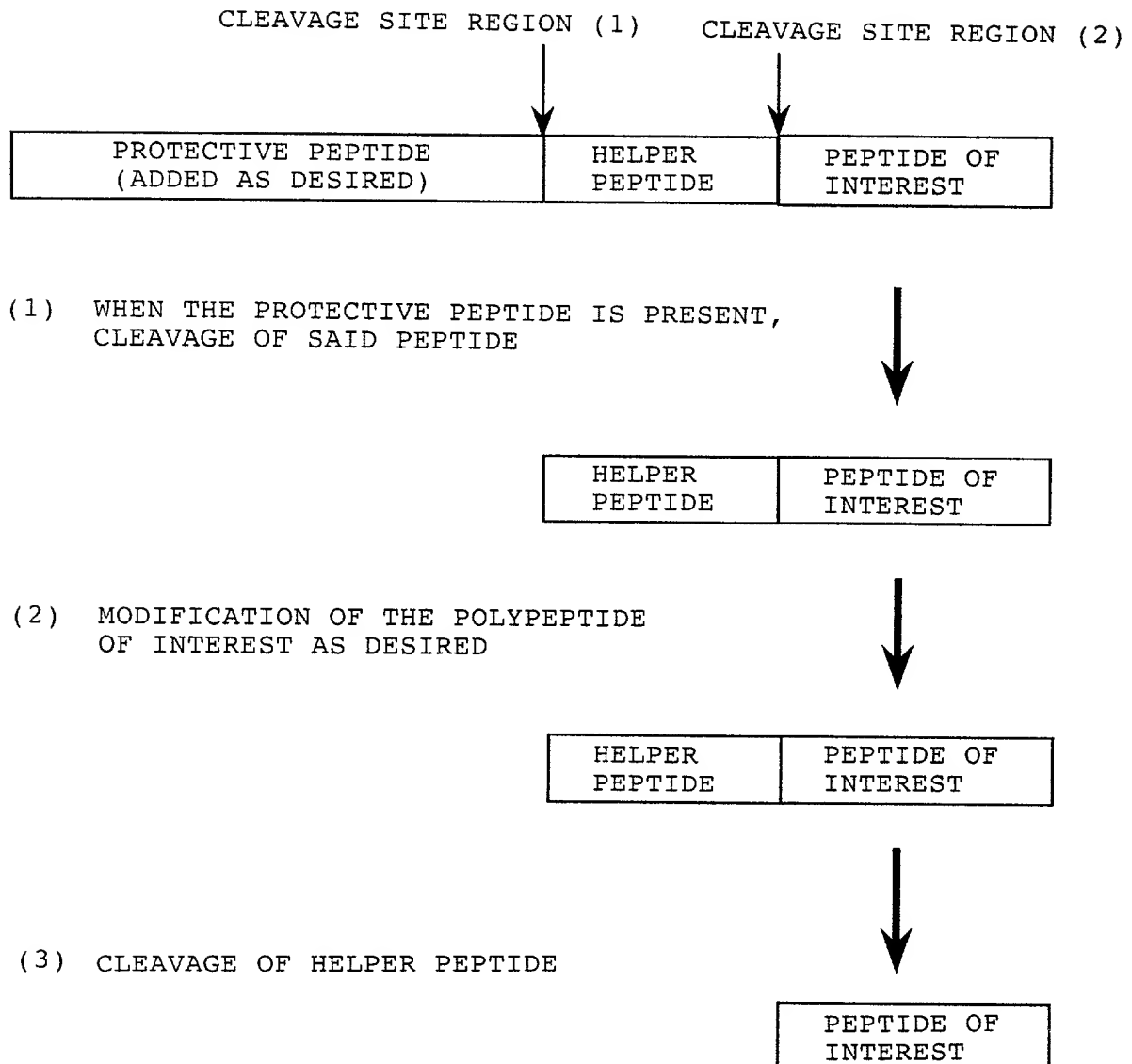


Fig. 2

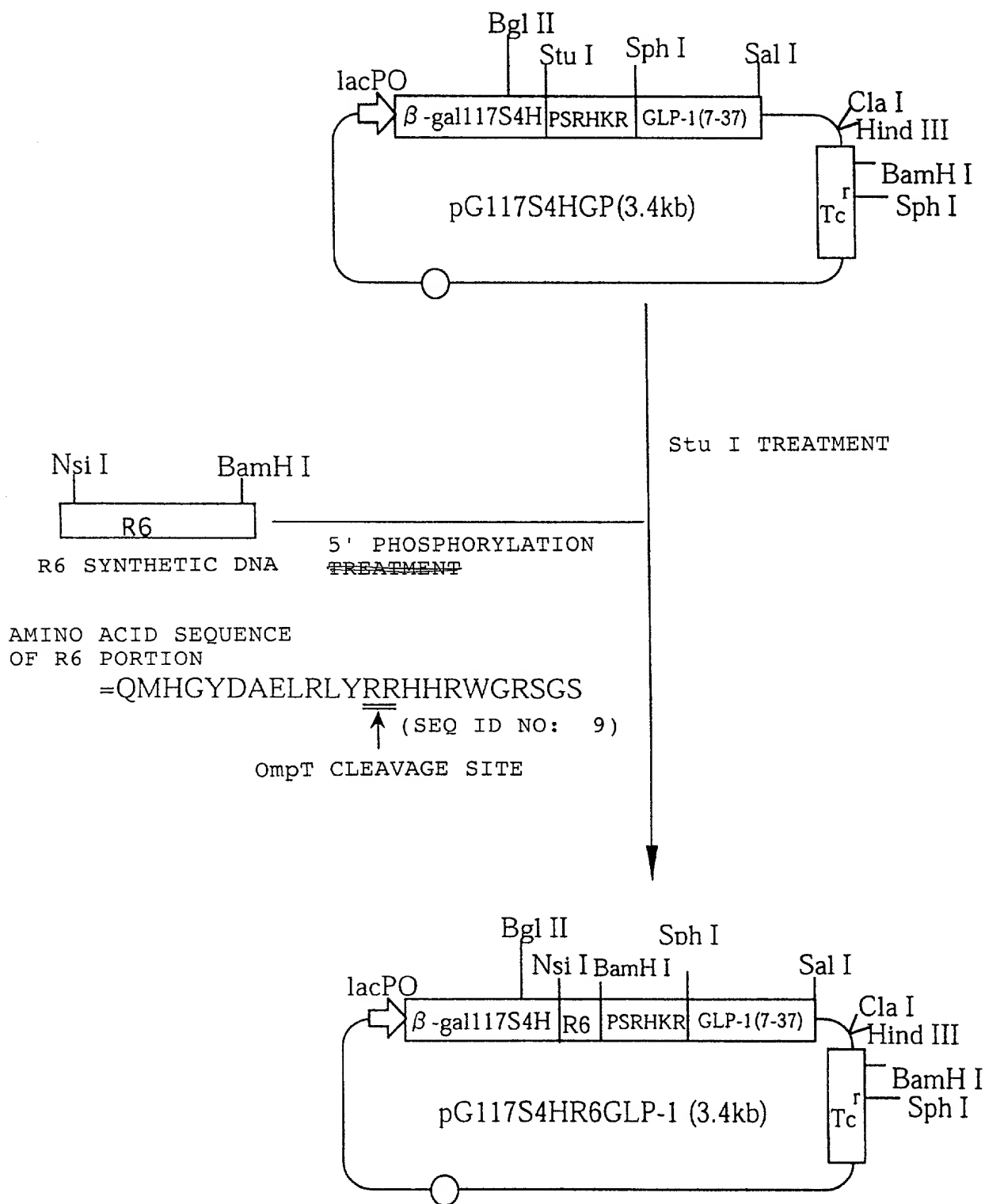
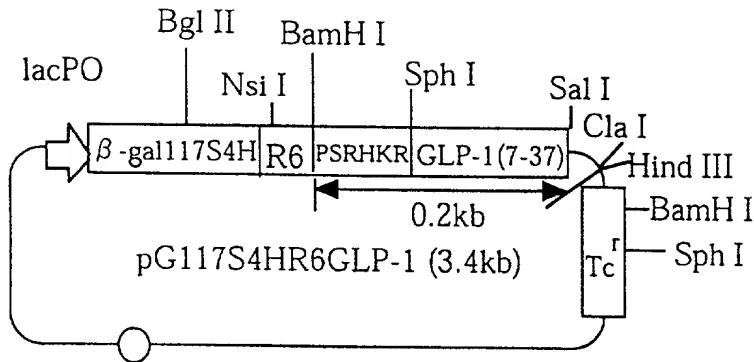
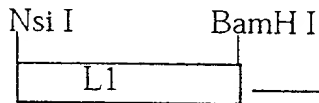
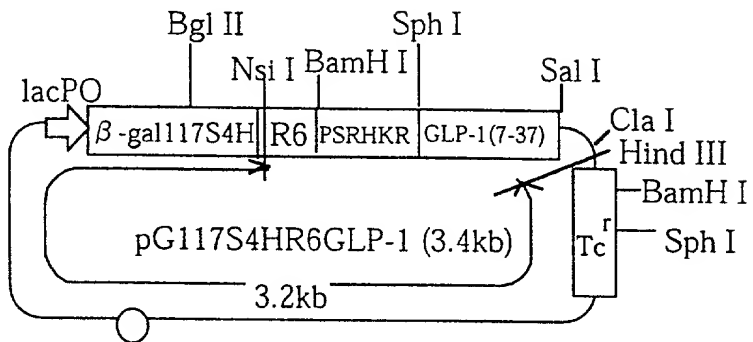


Fig. 3



BamH I, Hind III TREATMENT
RECOVER 0.2 kb FRAGMENT
(DNA FRAGMENT B)



L1 SYNTHETIC DNA

5' PHOSPHORYLATION
TREATMENT

AMINO ACID SEQUENCE
OF L1 PORTION

=QMhGYDAELRLYRRHHGSGS

(SEQ ID NO: 10)

OmpT CLEAVAGE SITE

Nsi I, Hind III TREATMENT
RECOVER 3.2 kb FRAGMENT
(DNA FRAGMENT A)

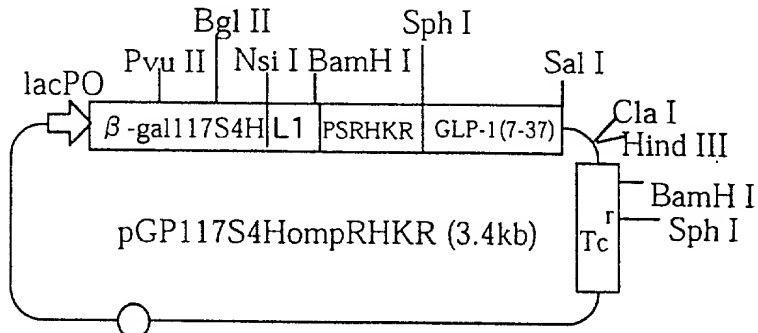


Fig. 4

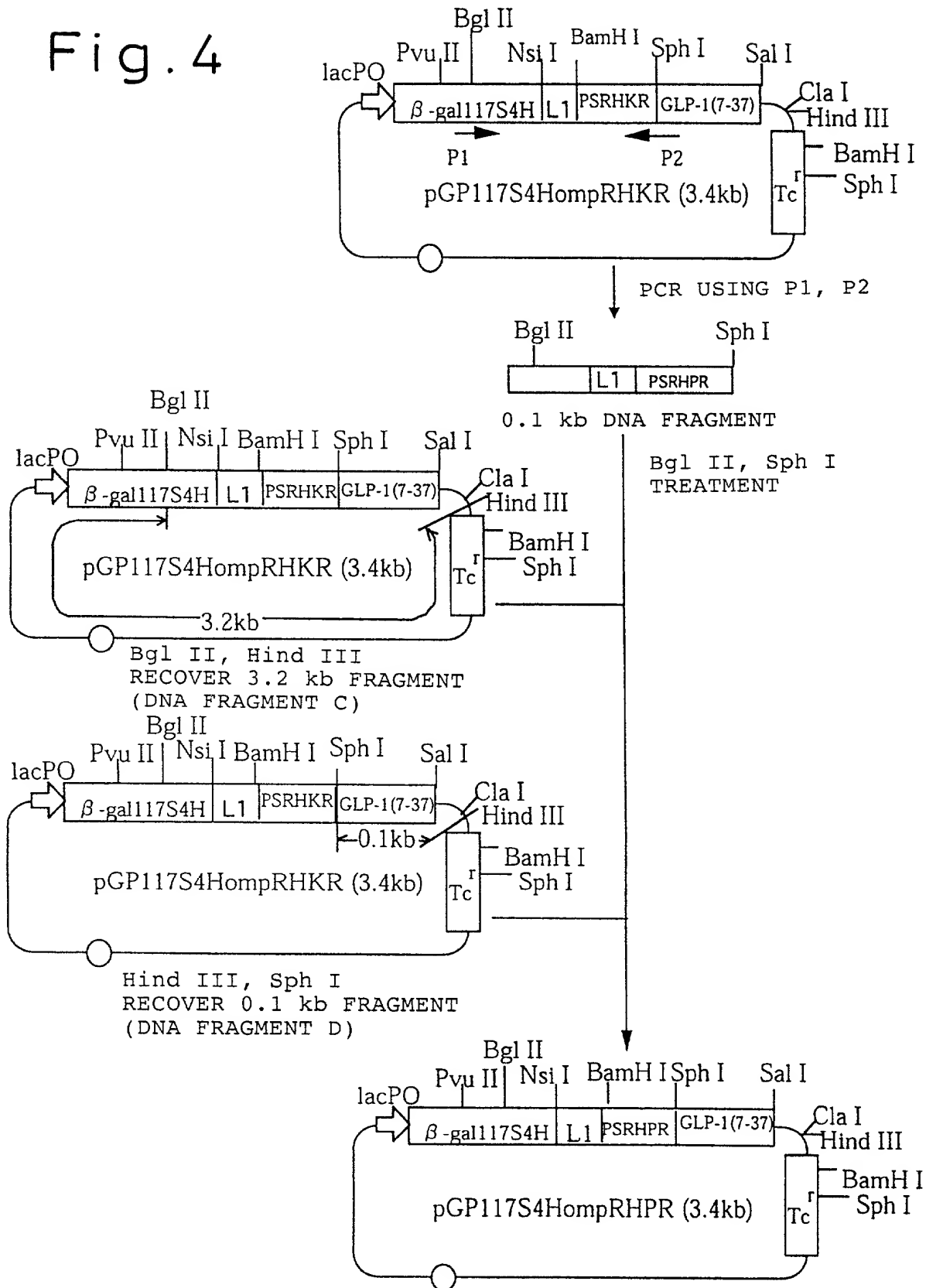


Fig. 5

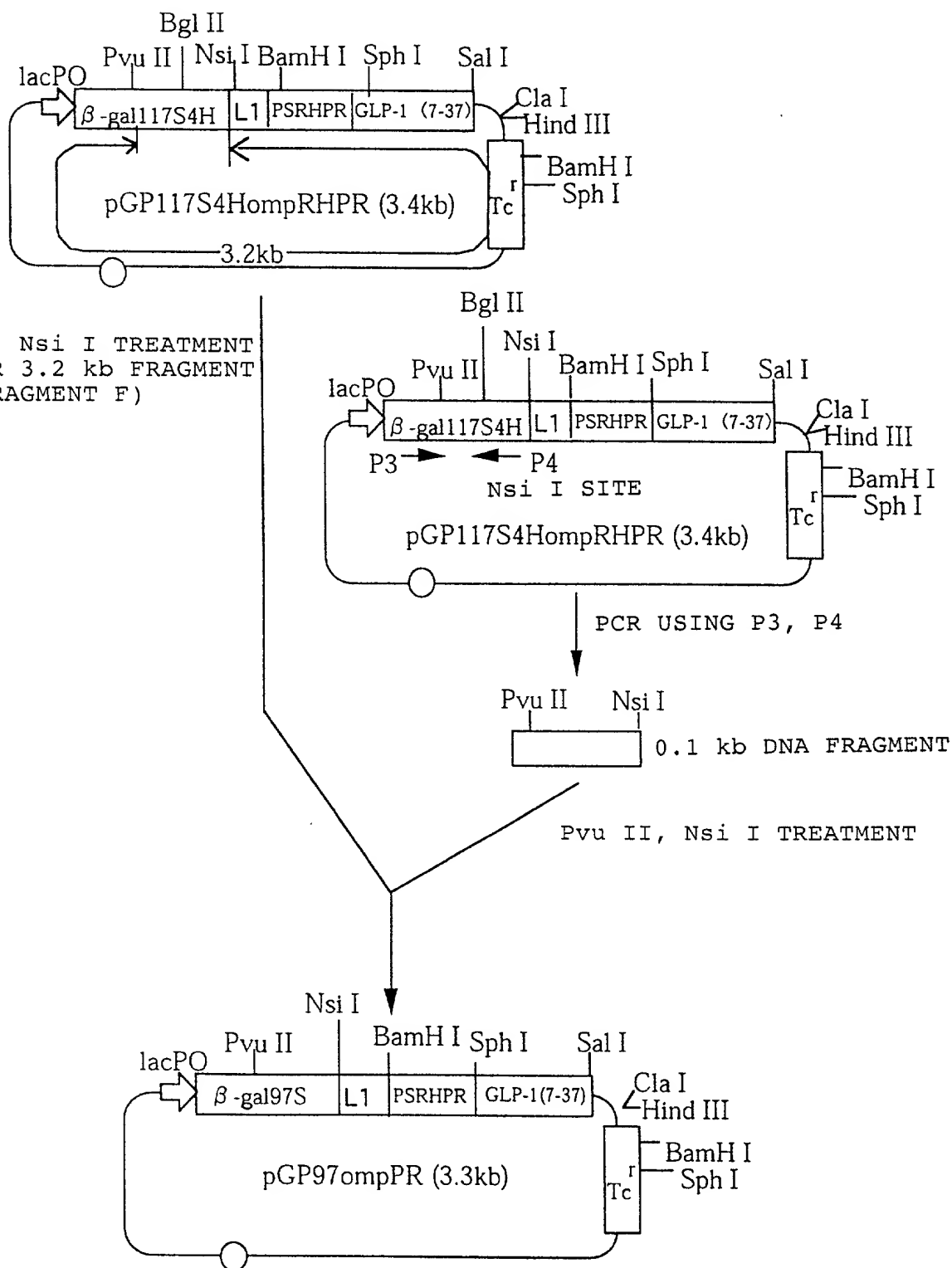


Fig.6

R6 SEQUENCE

5' CAG ATG CAT GGT TAT GAC GCG GAG CTC CGG CTG TAT CGC CGT CAT CAC CGG
3' GTC TAC GTA CCA ATA CTG CGC CTC GAG GCC GAC ATA GCG GCA GTA GTG GCC

CORRESPONDING

Gln Met His Gly Tyr Asp Ala Glu Leu Arg Leu Tyr Arg Arg His His Arg

AMINO ACID SEQUENCE

(SEQ ID NO: 11) (SEQ ID NO: 12)

TGG GGT CGT TCC GGA TCC 3'

ACC CCA GCA AGG CCT AGG 5'

Trp Gly Arg Ser Gly Ser

6/24

L1 SEQUENCE

5' T GGT TAT GAC GCG GAG CTC CGC CTG TAT CGC CGT CAT CAC GGT TCC G
3' ACGTA CCA ATA CTG CGC CTC GAG GCG GAC ATA GCG GCA GTA GTG CCA AGG CCT AG 5'

(SEQ ID NO: 13)
(SEQ ID NO: 14)

P1 PRIMER SEQUENCE

5' GAC TCA GAT CTT CCT GAG GCC GAT 3' (SEQ ID NO: 15)

P2 PRIMER SEQUENCE

5' AAA GGT ACC TTC CGC ATG CCG CGG ATG TCG AGA AGG 3' (SEQ ID NO: 16)

P3 PRIMER SEQUENCE

5' AGG CCA GGA ACC GTA AAA AG 3' (SEQ ID NO: 17)

P4 PRIMER SEQUENCE

5' AAA ATG CAT CGC ATC GTA ACC GTG CAT CT 3' (SEQ ID NO: 18)

66-2446-1

09/402093

Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Lys	15
Asp Trp Asp Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala	30
His Pro Pro Phe Ala Ser Trp Arg Asn Ser Asp Asp Ala Arg Thr	45
Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg	60
Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Ala Ser Leu Leu	75
Glu Ser Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn	90
Trp Gln Met His Gly Tyr Asp Ala Met His Gly Tyr Asp Ala Glu	105
Leu Arg Leu Tyr Arg <u>Arg His His Gly Ser Gly Ser Pro Ser Arg</u>	120
<u>His Pro Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser</u>	135
<u>Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val</u>	150
<u>Lys Gly Arg Gly</u>	

154

AMINO ACID SEQUENCE OF FUSION PROTEIN (GP97ompPR)
 ENCODED BY pGP97ompPR

Fig.8

lac PO

CCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCG

1

GATAACAATTTACACAGGAAACAGCT ATG ACC ATG ATT ACG GAT TCA CTG GCC
Met Thr Met Ile Thr Asp Ser Leu Ala

GTC GTT TTA CAA CGT AAA GAC TGG GAT AAC CCT GGC GTT ACC CAA CTT
Val Val Leu Gln Arg Lys Asp Trp Asp Asn Pro Gly Val Thr Gln Leu

AAT CGC CTT GCA GCA CAT CCC CCT TTC GCC AGC TGG CGT AAT AGC GAC
Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Asp

GAC GCC CGC ACC GAT CGC CCT TCC CAA CAG TTG CGC AGC CTG AAT GGC
Asp Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly

GAA TGG CGC TTT GCC TGG TTT CCG GCA CCA GAA GCG GTG CCG GCA AGC
Glu Trp Arg Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Ala Ser

TTG CTG GAG TCA GAT CTT CCT GAG GCC GAT ACT GTC GTC GTC CCC TCA
Leu Leu Glu Ser Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser

AAC TGG CAG ATG CAC GGT TAC GAT GCG ATG CAT GGT TAT GAC GCG GAG
Asn Trp Gln Met His Gly Tyr Asp Ala Met His Gly Tyr Asp Ala Glu

CTC CGC CTG TAT CGC CGT CAT CAC GGT TCC GGA TCC CCT TCT CGA CAT
Leu Arg Leu Tyr Arg Arg His His Gly Ser Gly Ser Pro Ser Arg His

CCG CGG CAT GCG GAA GGT ACC TTT ACC AGC GAT GTG AGC TCG TAT CTG
Pro Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu

GAA GGT CAG GCG GCA AAA GAA TTC ATC GCG TGG CTG GTG AAA GGC CGT
Glu Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg

462

GGT TAA GTCGAC AGCCCGCCTAATGAGCGGGCTTTTTTTTCTCGGAATTAATTCTCATGT
Gly ***

STOP CODON

TTGACAGCTTATCATCGATAAGCTTTA

(SEQ ID NO: 19)

Fig. 9

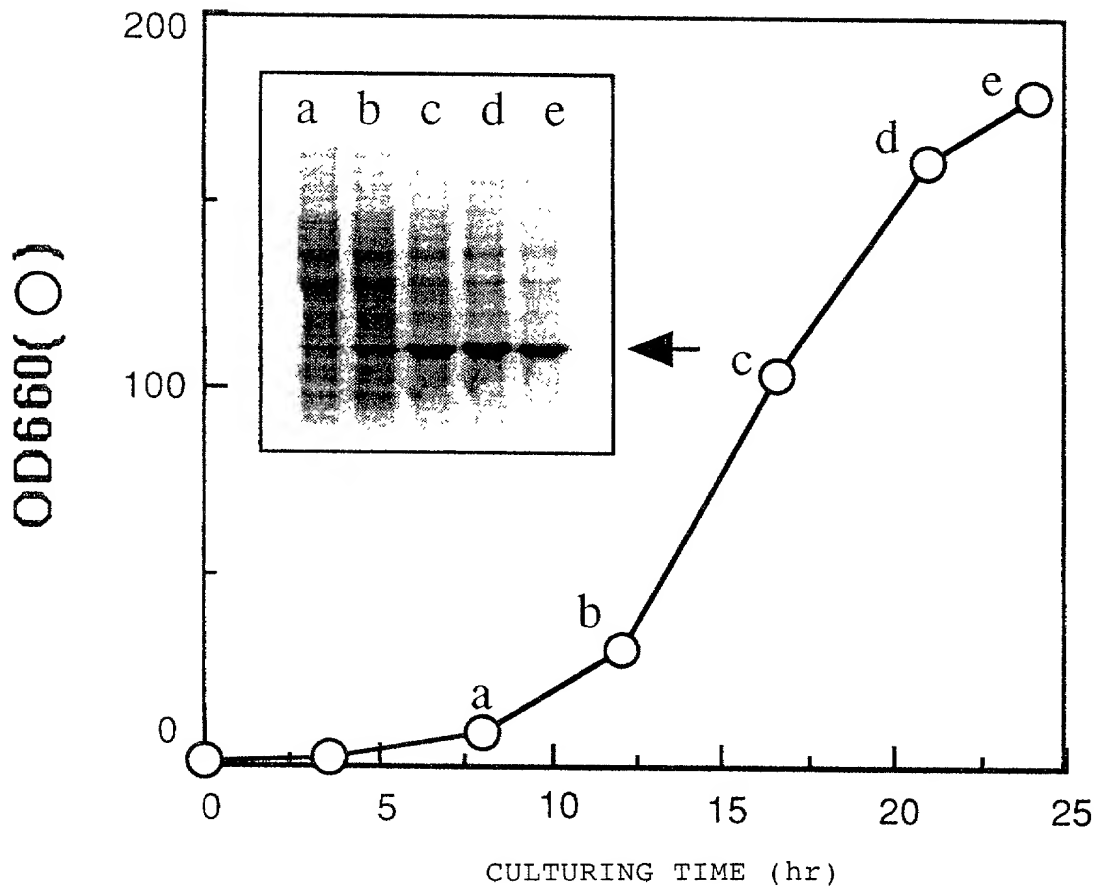


Fig.10

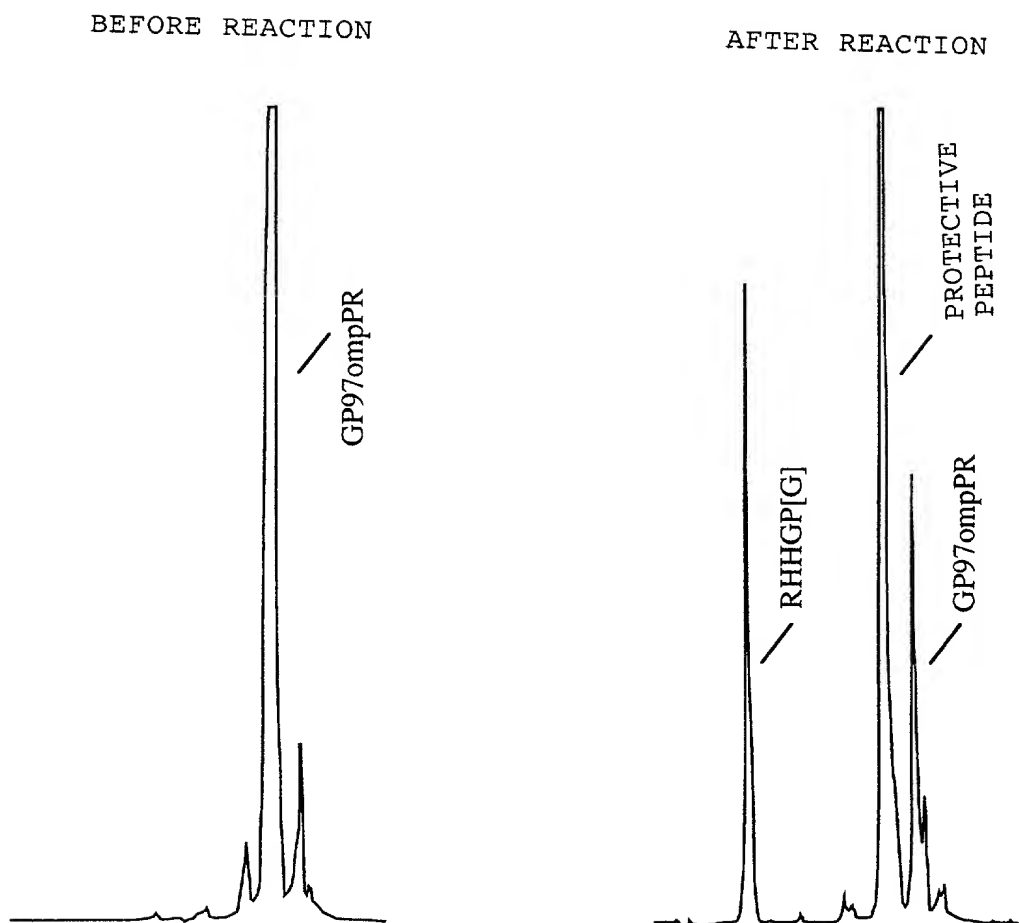


Fig.11

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Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Lys 15
Asp Trp Asp Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala 30
His Pro Pro Phe Ala Ser Trp Arg Asn Ser Asp Asp Ala Arg Thr 45
Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg 60
Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Ala Ser Leu Leu 75
Glu Ser Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn 90
Trp Gln Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr 105
Tyr Pro Ile Thr Val Asn Pro Pro Phe Val Pro Thr Glu Pro His 120
His His His His Gly Gly Arg Gln Met His Gly Tyr Asp Ala Glu 135
Leu Arg Leu Tyr Arg Arg His His Arg Trp Gly Arg Ser Gly Ser 150
Pro Ser Arg His Lys Arg His Ala Glu Gly Thr Phe Thr Ser Asp 165
Val Ser Ser Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile Ala 180
Trp Leu Val Lys Gly Arg Gly

```

(SEQ ID NO: 21)

AMINO ACID SEQUENCE OF FUSION PROTEIN
 ENCODED BY pG117S4HR6GLP-1

PE 32 3 091075512

Fig.12

Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Lys 15
 Asp Trp Asp Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala 30
 His Pro Pro Phe Ala Ser Trp Arg Asn Ser Asp Asp Ala Arg Thr 45
 Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg 60
 Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Ala Ser Leu Leu 75
 Glu Ser Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn 90
 Trp Gln Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr 105
 Tyr Pro Ile Thr Val Asn Pro Pro Phe Val Pro Thr Glu Pro His 120
 His His His His Gly Gly Arg Gln Met His Gly Tyr Asp Ala Glu 135
 Leu Arg Leu Tyr Arg Arg His His Gly Ser Gly Ser Pro Ser Arg 150
His Lys Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser 165
Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val 180
Lys Gly Arg Gly

(SEQ ID NO: 22)

AMINO ACID SEQUENCE OF FUSION PROTEIN
 ENCODED BY pGP117S4HompRHKR

Fig.13

Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Lys 15
 Asp Trp Asp Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala 30
 His Pro Pro Phe Ala Ser Trp Arg Asn Ser Asp Asp Ala Arg Thr 45
 Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg 60
 Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Ala Ser Leu Leu 75
 Glu Ser Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn 90
 Trp Gln Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr 105
 Tyr Pro Ile Thr Val Asn Pro Pro Phe Val Pro Thr Glu Pro His 120
 His His His His Gly Gly Arg Gln Met His Gly Tyr Asp Ala Glu 135
 Leu Arg Leu Tyr Arg Arg His His Gly Ser Gly Ser Pro Ser Arg 150
His Pro Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser 165
Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val 180
Lys Gly Arg Gly

(SEQ ID NO: 23)

AMINO ACID SEQUENCE OF FUSION PROTEIN
 ENCODED BY pGP117S4HompRHPR

Fig.14

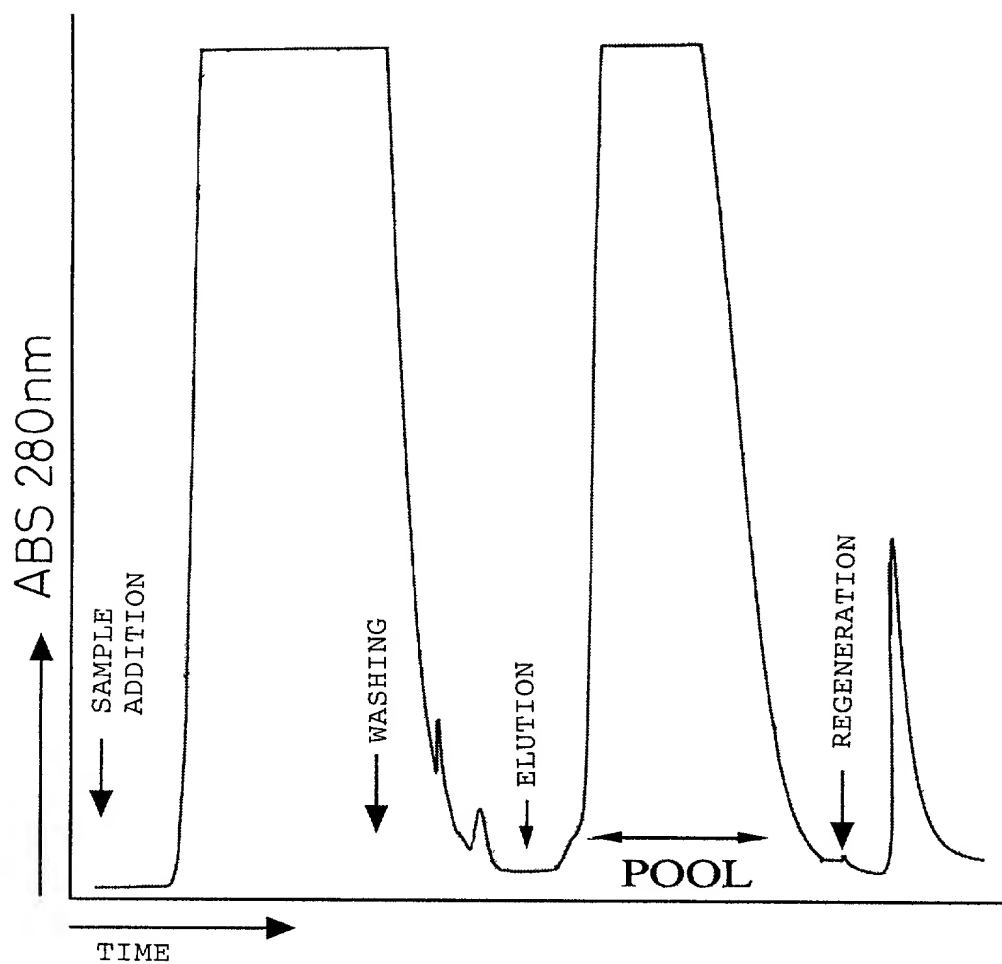


Fig.15

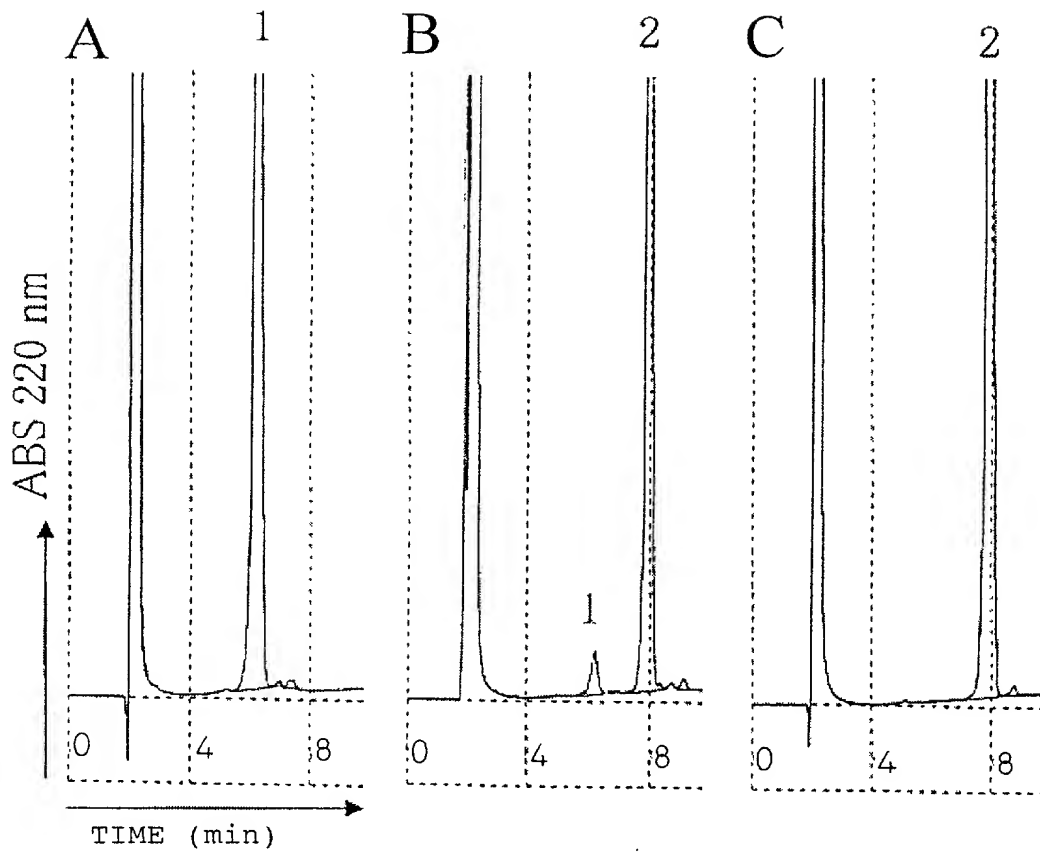


Fig.16

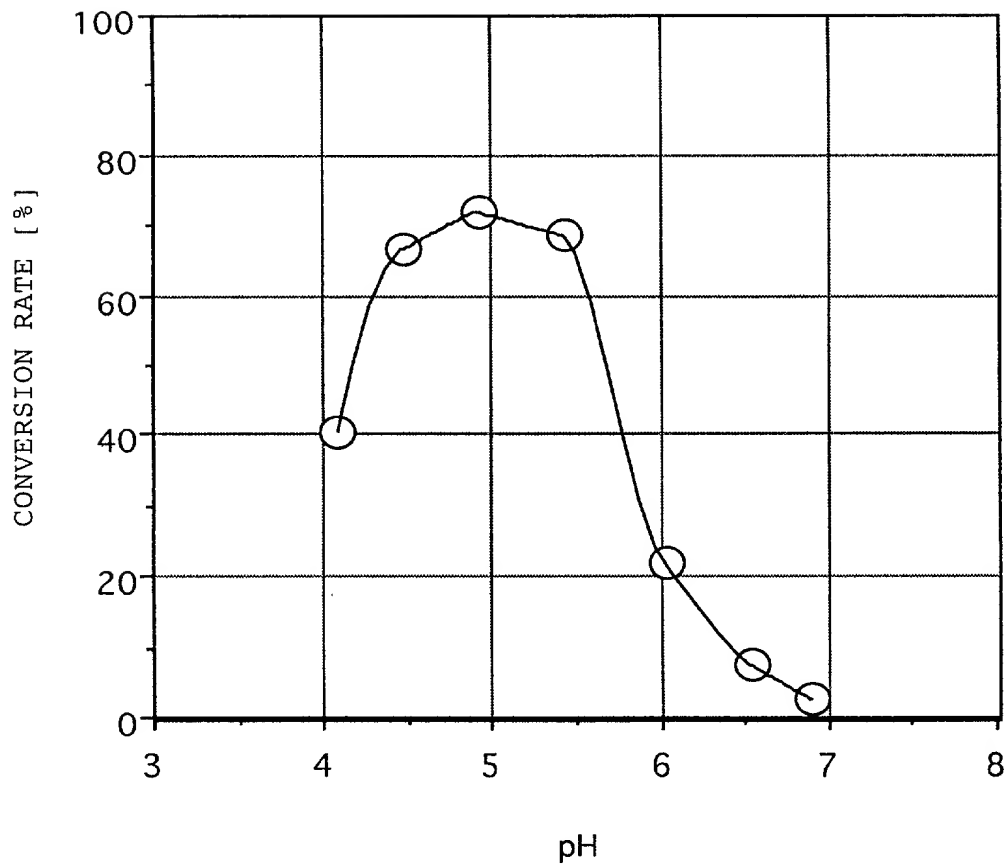
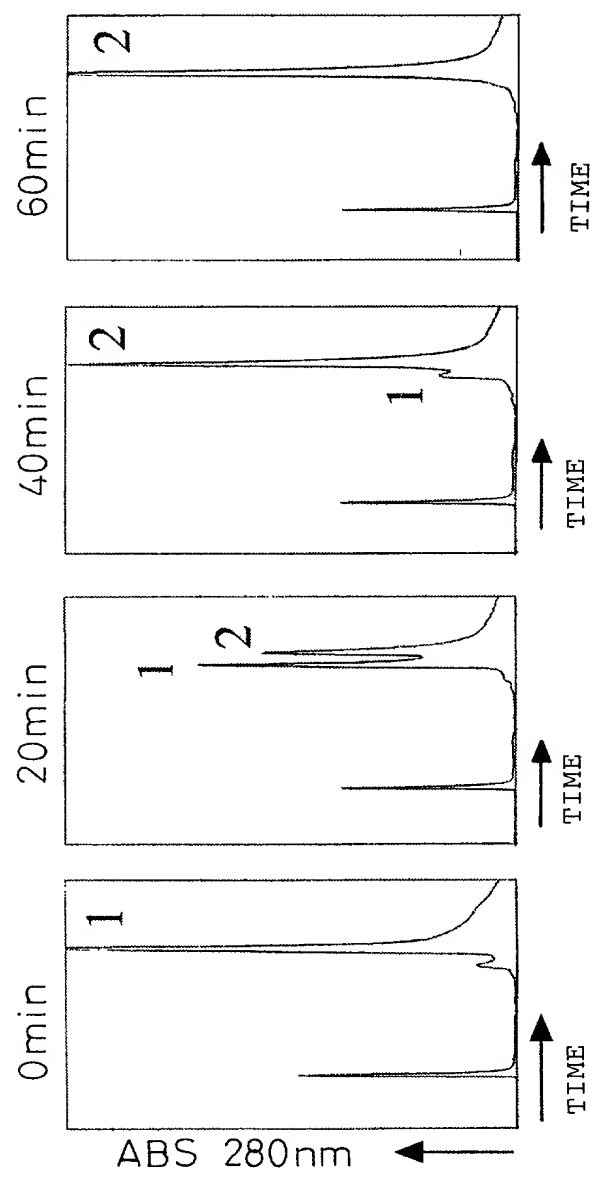


Fig.17



09/402093

Fig.18

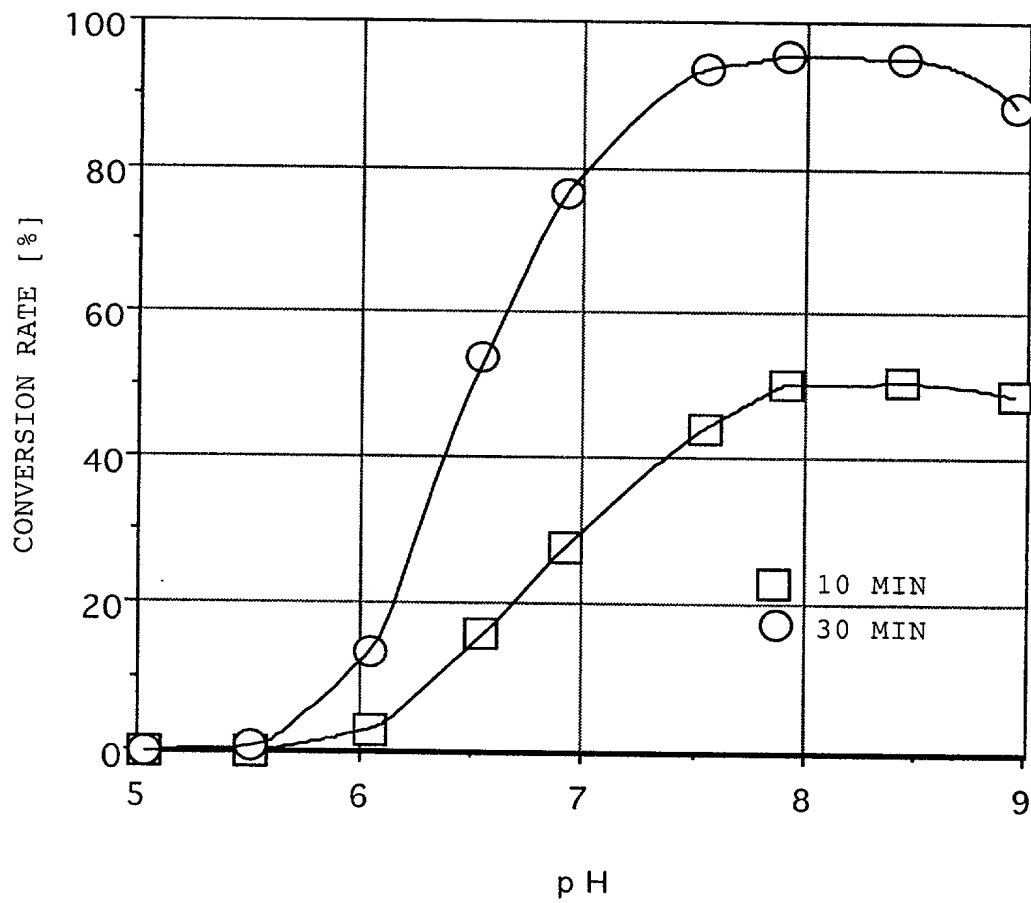


Fig.19

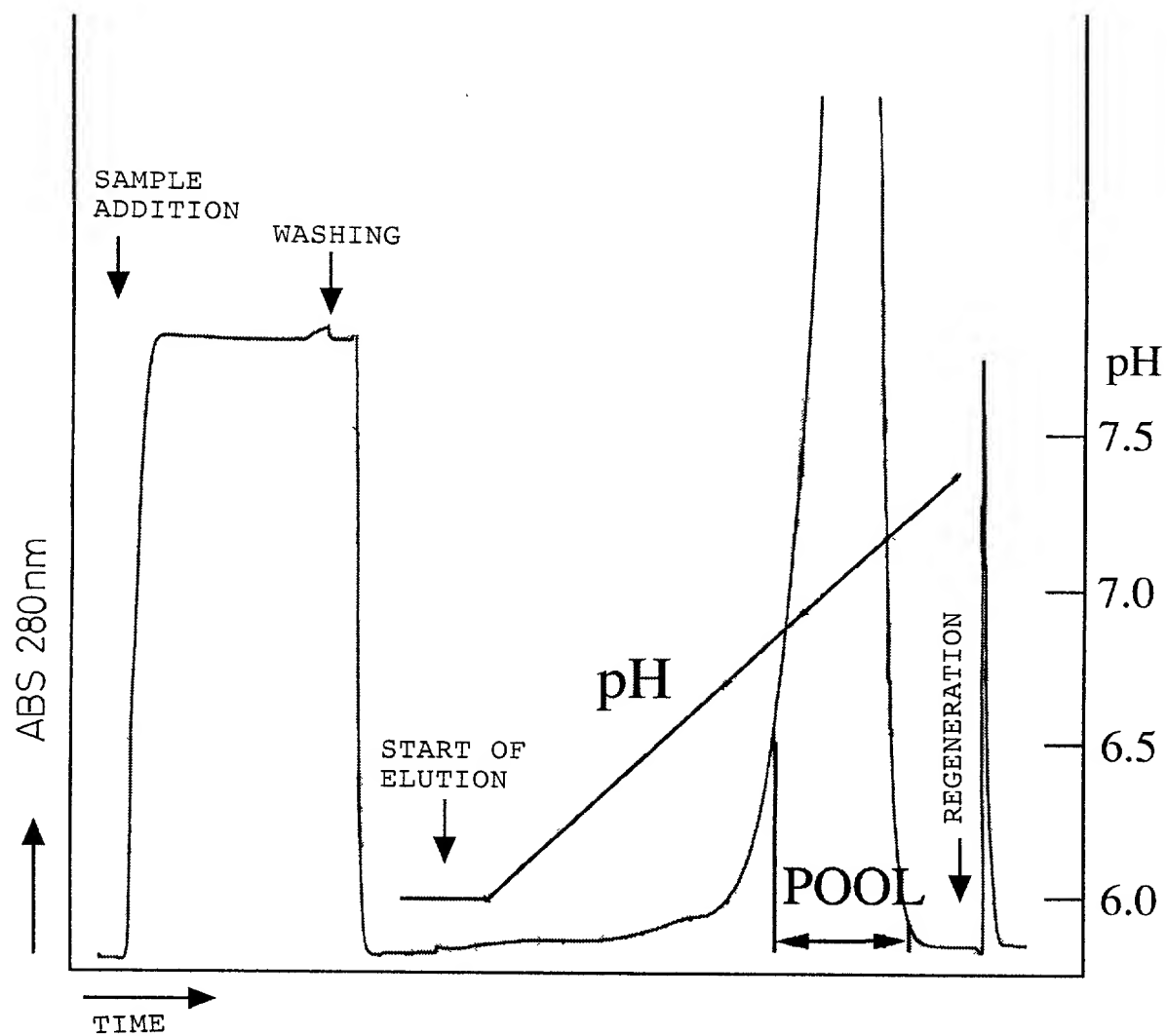


Fig.20

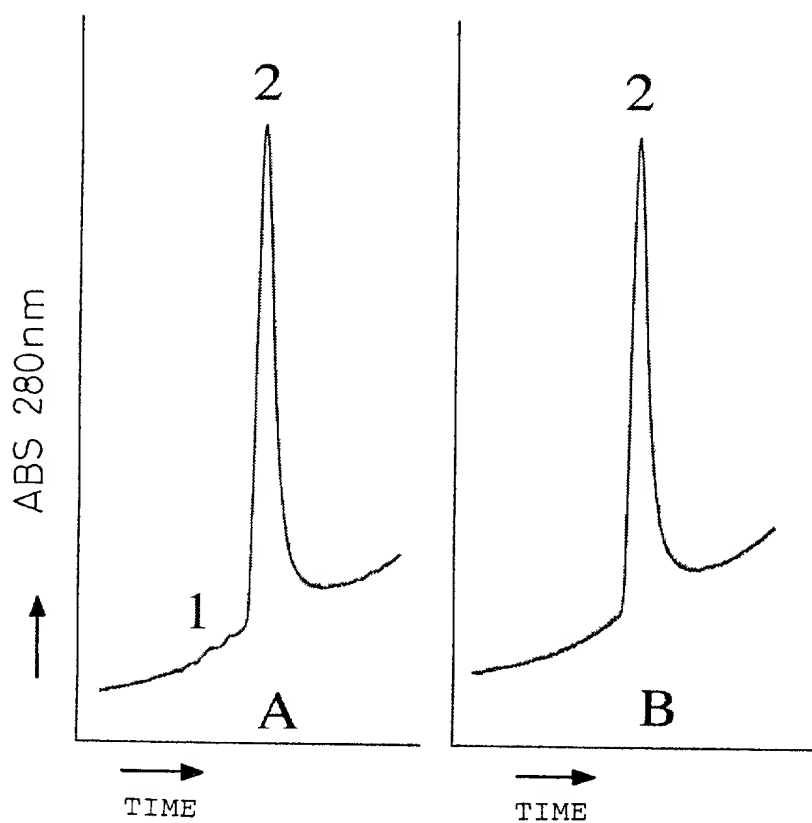


Fig.21

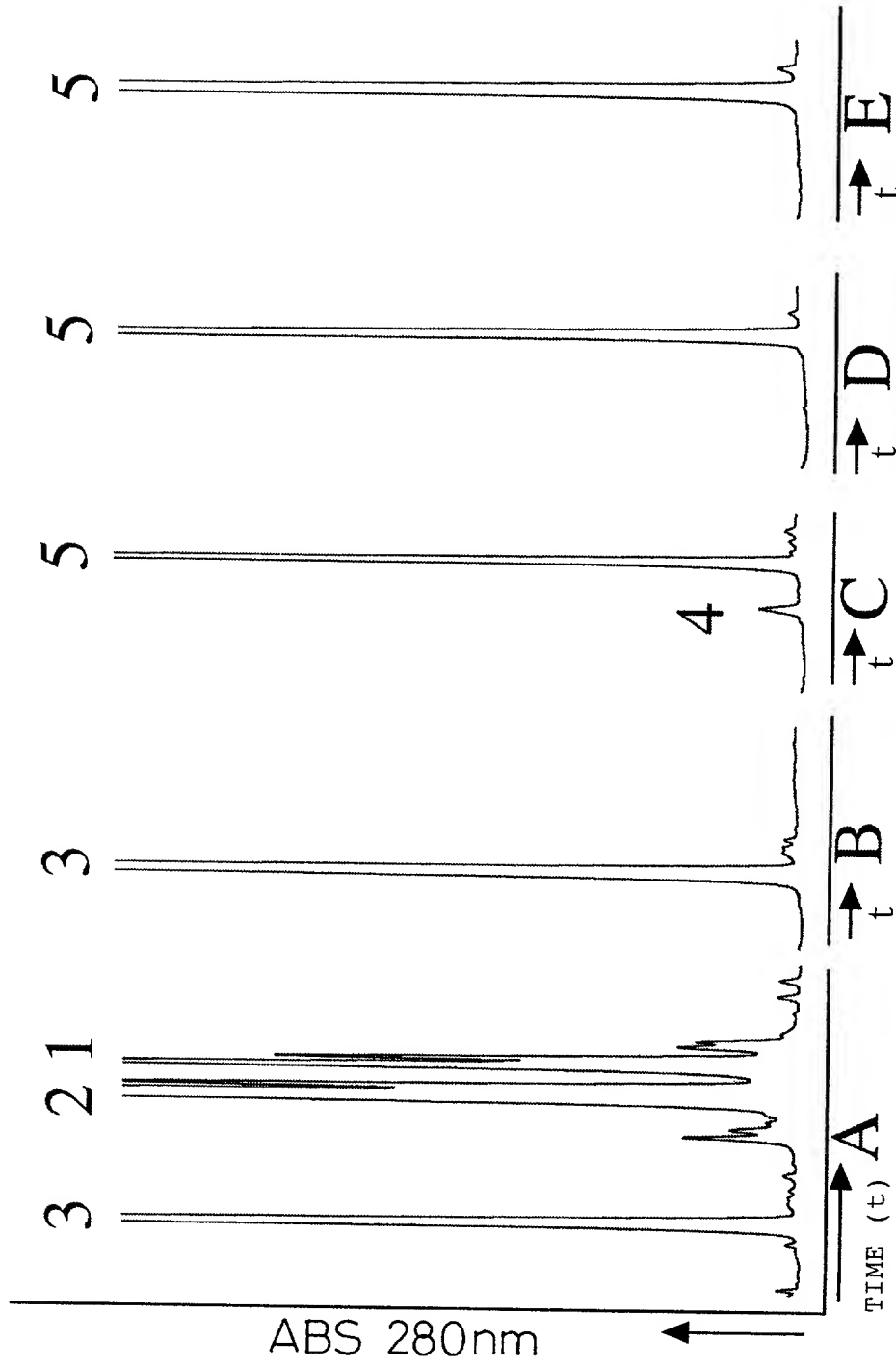


Fig.22

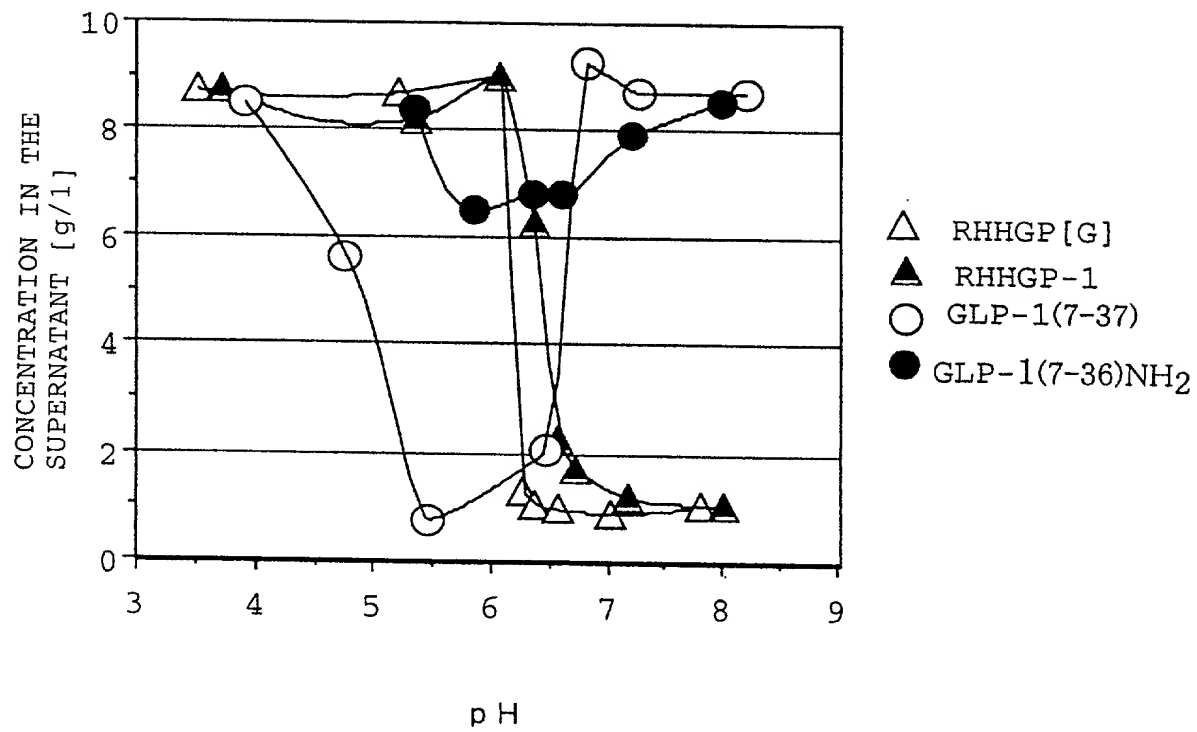
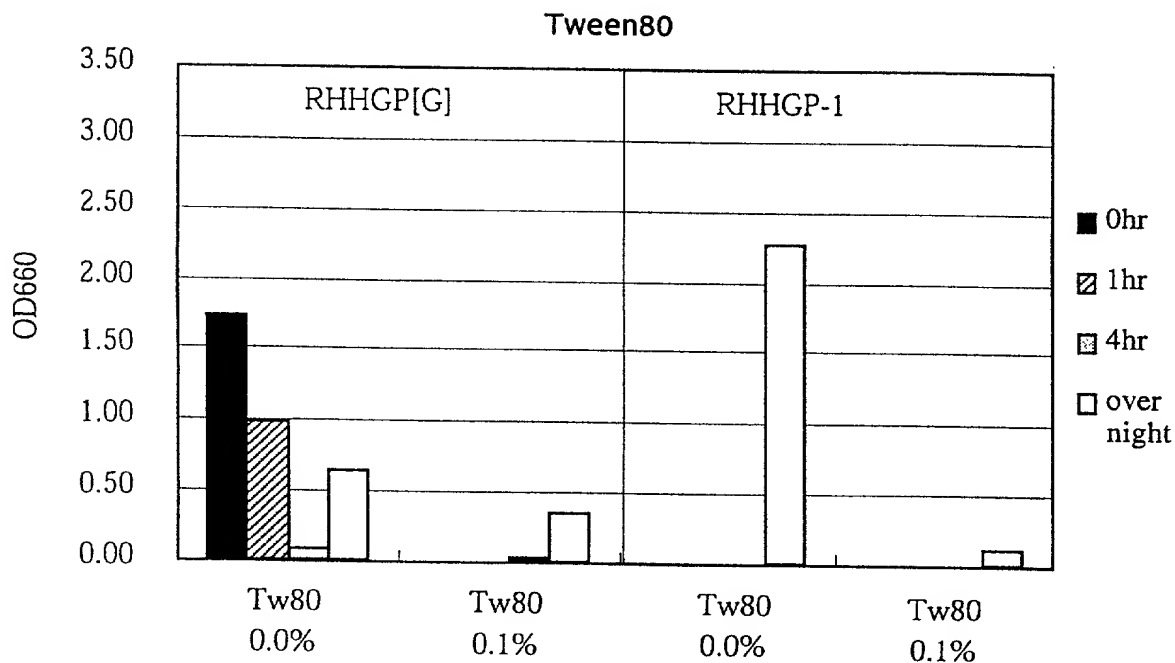


Fig.23

A



B

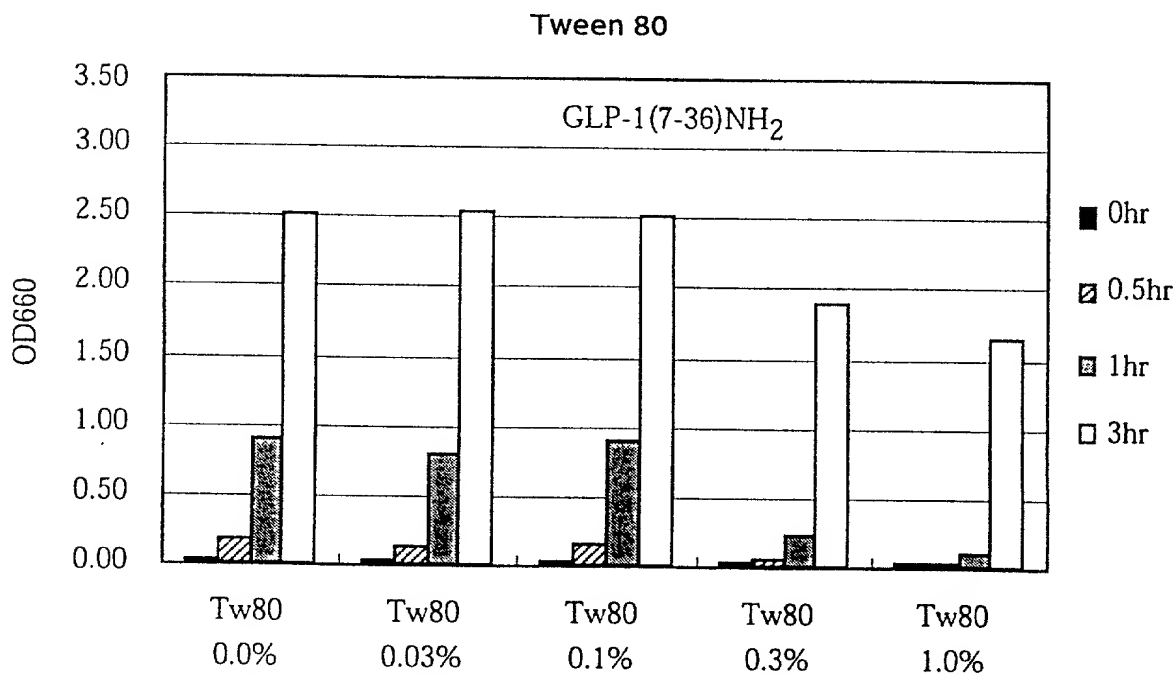
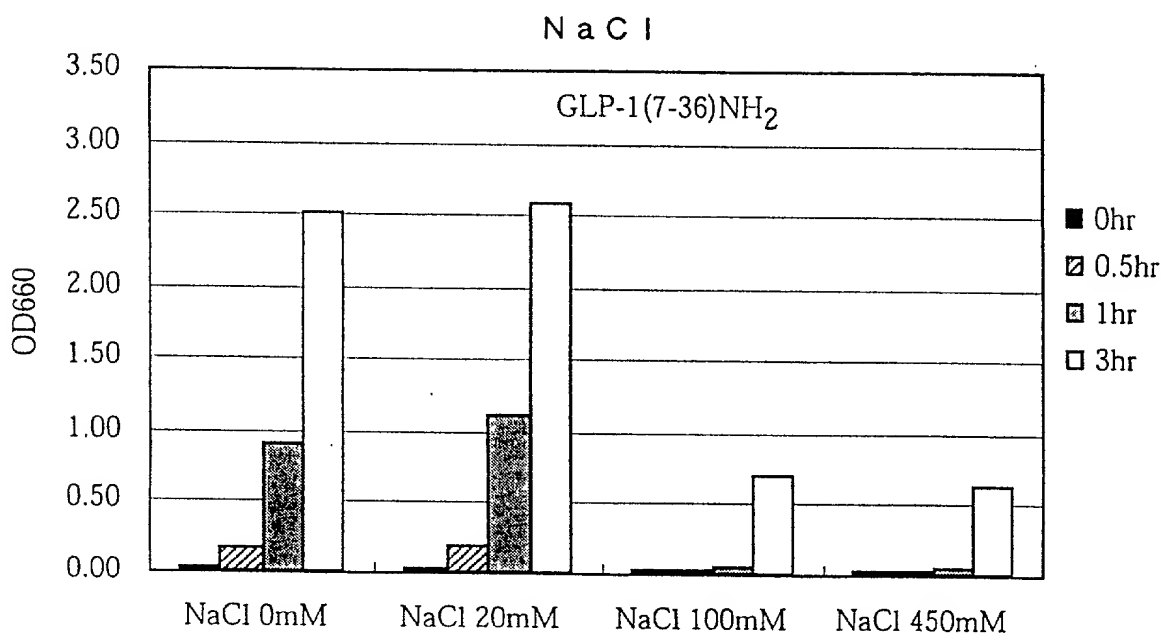
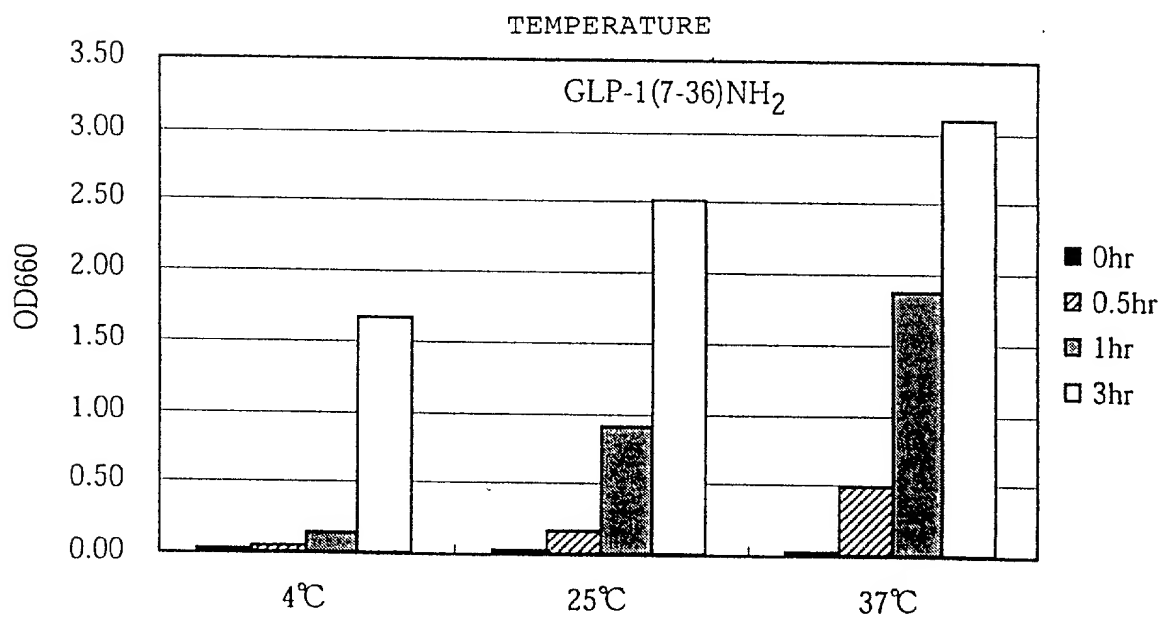


Fig. 24

A



B



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特許出願宣言書及び委任状

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日本語宣言書

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As a below named inventor, I hereby declare that:

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My residence, post office address and citizenship are as stated next to my name.

下記の名称の発明に関して請求範囲に記載され、特許出願している発明内容について、私が最初かつ唯一の発明者（下記の氏名が一つの場合）もしくは最初かつ共同発明者であると（下記の名称が複数の場合）信じています。

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

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the specification of which is attached hereto unless the following box is checked:

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☐ was filed on January 29, 1999
as United States Application Number or
PCT International Application Number
PCT/JP99/00406 and was amended on _____
(if applicable).

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Prior Foreign Application(s)

外国での先行出願

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(Number) (Country)
(番号) (国名)

(Number) (Country)
(番号) (国名)

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日以降で本出願書の日本国内または特許協力条約国際提出
日までの期間中に入手された、連邦規則法典第37編1条5
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(Application No.) (Filing Date)
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(Application No.) (Filing Date)
(出願番号) (出願日)

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の有効性が失われることを認識し、よってここに上記のごと
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Priority Not Claimed
優先権主張なし

30/January/1998
(Day/Month/Year Filed)
(出願年月日)

(Day/Month/Year Filed)
(出願年月日)

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(Application No.) (Filing Date)
(出願番号) (出願日)

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(Status: Patented, Pending, Abandoned)
(現況: 特許許可済、係属中、放棄済)

(Status: Patented, Pending, Abandoned)
(現況: 特許許可済、係属中、放棄済)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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委任状: 私は下記の発明者として、本出願に関する一切の手続きを米特許商標局に対して遂行する弁理士または代理人として、下記の者を指名いたします。(弁護士、または代理人の氏名及び登録番号を明記のこと)

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith (list name and registration number)

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Bruce J. Boggs, Jr. 32,344

William H. Benz 25,952
Peter K. Skiff 31,917
Richard J. McGrath 29,195
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Gerald F. Swiss 30,113
Michael J. Ure 33,089
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国籍	Citizenship	<u>Japanese</u>
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		<u>Japan</u>
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日付	Date	<u>September 9, 1999</u>
住所	Residence	<u>Tatebayashi-shi, Gunma, Japan JPX</u>
国籍	Citizenship	<u>Japanese</u>
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		<u>Gunma 374-0038, Japan</u>

(第三以降の共同発明者についても同様に記載し、署名をすること)

(Supply similar information and signature for third and subsequent joint inventors.)

3-00

第三共同発明者	Full name of third joint inventor, if any <u>Yuji Suzuki</u>		
第三共同発明者	日付	Third inventor's signature <u>Yuji Suzuki</u>	Date September 9, 1999
住 所	Residence <u>Ashikaga-shi, Tochigi, Japan JPX</u>		
国 籍	Citizenship Japanese		
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第四共同発明者	Full name of fourth joint inventor, if any		
第四共同発明者	日付	Fourth inventor's signature	Date
住 所	Residence		
国 籍	Citizenship		
私書箱	Post Office Address		

第五共同発明者	Full name of fifth joint inventor, if any		
第五共同発明者	日付	Fifth inventor's signature	Date
住 所	Residence		
国 籍	Citizenship		
私書箱	Post Office Address		
第六共同発明者	Full name of sixth joint inventor, if any		
第六共同発明者	日付	Sixth inventor's signature	Date
住 所	Residence		
国 籍	Citizenship		
私書箱	Post Office Address		

(第七以降の共同発明者についても同様に
記載し、署名をすること)

(Supply similar information and signature for
seventh and subsequent joint inventors.)

SEQUENCE LISTING

<110> Suntory Limited

<120> Process for producing peptides using a
 helper peptide

<130> F962

<150> JP 10-032272

<151> 1998-01-30

<160> 24

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<210> 2

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<210> 3

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence containing a site cleaved by
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<210> 4

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<212> PRT

<213> Artificial Sequence

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<400> 4

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<211> 6

<212> PRT

<213> Artificial Sequence

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<223> Amino acid sequence of helper peptide

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<210> 7

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<223> Amino acid sequence of helper peptide

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<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Amino acid sequence containing a site cleaved by
Kex2 protease

<400> 8

Ser Asp His Lys Arg

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<210> 9

<211> 23

<212> PRT

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<223> Amino acid sequence of containing a position
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<400> 9

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Arg Trp Gly Arg Ser Gly Ser

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<210> 10

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence containing a position cleaved
by OmpT

<400> 10

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 1 5 10 15

Gly Ser Gly Ser
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<210> 11

<211> 69

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<213> Artificial Sequence

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<223> Nucleotide sequence coding for an amino acid
 sequence containing a site cleaved by OmpT

<400> 11

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Gln Met His Gly Tyr Asp Ala Glu Leu Arg Leu Tyr Arg Arg His His
 1 5 10 15

cgg tgg ggt cgt tcc gga tcc 69

Arg Trp Gly Arg Ser Gly Ser
 20

<210> 12

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence containing a site cleaved by
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<400> 12

Gln Met His Gly Tyr Asp Ala Glu Leu Arg Leu Tyr Arg Arg His His
 1 5 10 15

Arg Trp Gly Arg Ser Gly Ser
 20

<210> 13
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding for an amino acid
sequence containing a site cleaved by OmpT

<400> 13
tggttatgac gaggagctcc gcctgtatcg ccgtcatcac gggtccg 47

<210> 14
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence coding for an amino acid
sequence containing a site cleaved by OmpT

<400> 14
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<210> 15
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<212> DNA
<213> Artificial Sequence

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<400> 15
gactcagatc ttcttgaggc cgat 24

<210> 16
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
aaaggtacct tccgcatgcc gcggatgtcg agaagg

36

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<220>
<223> Primer

<400> 17
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<210> 18
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
aaaatgcata gcatcgtaac cgtgcatct

29

<210> 19

<211> 627
 <212> DNA
 <213> Artificial Sequence

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 <223> Nucleotide sequence coding for a fusion protein
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 aatttcacac aggaacacgc t atg acc atg att acg gat tca ctg gcc gtc 111
 Met Thr Met Ile Thr Asp Ser Leu Ala Val
 1 5 10
 gtt tta caa cgt aaa gac tgg gat aac cct ggc gtt acc caa ctt aat 159
 Val Leu Gln Arg Lys Asp Trp Asp Asn Pro Gly Val Thr Gln Leu Asn
 15 20 25
 cgc ctt gca gca cat ccc cct ttc gcc agc tgg cgt aat agc gac gac 207
 Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Asp Asp
 30 35 40
 gcc cgc acc gat cgc cct tcc caa cag ttg cgc agc ctg aat ggc gaa 255
 Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu
 45 50 55
 tgg cgc ttt gcc tgg ttt ccg gca cca gaa gcg gtg ccg gca agc ttg 303
 Trp Arg Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Ala Ser Leu
 60 65 70
 ctg gag tca gat ctt cct gag gcc gat act gtc gtc gtc ccc tca aac 351
 Leu Glu Ser Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn
 75 80 85 90
 tgg cag atg cac ggt tac gat gcg atg cat ggt tat gac gcg gag ctc 399
 Trp Gln Met His Gly Tyr Asp Ala Met His Gly Tyr Asp Ala Glu Leu
 95 100 105
 cgc ctg tat cgc cgt cat cac ggt tcc gga tcc cct tct cga cat ccg 447
 Arg Leu Tyr Arg Arg His His Gly Ser Gly Ser Pro Ser Arg His Pro
 110 115 120

cgg cat gcg gaa ggt acc ttt acc agc gat gtg agc tcg tat ctg gaa 495
 Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu
 125 130 135
 ggt cag gcg gca aaa gaa ttc atc gcg tgg ctg gtg aaa ggc cgt ggt 543
 Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
 140 145 150
 taagtcgaca gccgcgctaa tgagcgggct tttttttctc ggaattaatt ctcattgttg 603
 acagcttatc atcgataagc tttta 627

<210> 20
 <211> 154
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Amino acid sequence of a fusion protein comprising
 GLP-1, helper peptide and β -galactosidase
 protective peptide

<400> 20
 Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Lys Asp
 1 5 10 15
 Trp Asp Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro
 20 25 30
 Pro Phe Ala Ser Trp Arg Asn Ser Asp Asp Ala Arg Thr Asp Arg Pro
 35 40 45
 Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg Phe Ala Trp Phe
 50 55 60
 Pro Ala Pro Glu Ala Val Pro Ala Ser Leu Leu Glu Ser Asp Leu Pro
 65 70 75 80
 Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr
 85 90 95
 Asp Ala Met His Gly Tyr Asp Ala Glu Leu Arg Leu Tyr Arg Arg His
 100 105 110
 His Gly Ser Gly Ser Pro Ser Arg His Pro Arg His Ala Glu Gly Thr
 115 120 125

Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln Ala Ala Lys Glu
 130 135 140

Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
 145 150

<210> 21

<211> 187

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a fusion protein comprising
 GLP-1, helper peptide and β -galactosidase
 protective peptide

<400> 21

Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Lys Asp
 1 5 10 15
 Trp Asp Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro
 20 25 30
 Pro Phe Ala Ser Trp Arg Asn Ser Asp Asp Ala Arg Thr Asp Arg Pro
 35 40 45
 Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg Phe Ala Trp Phe
 50 55 60
 Pro Ala Pro Glu Ala Val Pro Ala Ser Leu Leu Glu Ser Asp Leu Pro
 65 70 75 80
 Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr
 85 90 95
 Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro Ile Thr Val Asn Pro
 100 105 110
 Pro Phe Val Pro Thr Glu Pro His His His His His Gly Gly Arg Gln
 115 120 125
 Met His Gly Tyr Asp Ala Glu Leu Arg Leu Tyr Arg Arg His His Arg
 130 135 140
 Trp Gly Arg Ser Gly Ser Pro Ser Arg His Lys Arg His Ala Glu Gly
 145 150 155 160

Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln Ala Ala Lys
165 170 175

Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
180 185

<210> 22

<211> 184

<212> PRT

<213> Artificial Sequence

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<223> Amino acid sequence of a fusion protein comprising
GLP-1, helper peptide and β -galactosidase
protective peptide

<400> 22

Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Lys Asp
1 5 10 15
Trp Asp Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro
20 25 30
Pro Phe Ala Ser Trp Arg Asn Ser Asp Asp Ala Arg Thr Asp Arg Pro
35 40 45
Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg Phe Ala Trp Phe
50 55 60
Pro Ala Pro Glu Ala Val Pro Ala Ser Leu Leu Glu Ser Asp Leu Pro
65 70 75 80
Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr
85 90 95
Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro Ile Thr Val Asn Pro
100 105 110
Pro Phe Val Pro Thr Glu Pro His His His His His Gly Gly Arg Gln
115 120 125
Met His Gly Tyr Asp Ala Glu Leu Arg Leu Tyr Arg Arg His His Gly
130 135 140
Ser Gly Ser Pro Ser Arg His Lys Arg His Ala Glu Gly Thr Phe Thr
145 150 155 160

Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile
165 170 175

Ala Trp Leu Val Lys Gly Arg Gly
180

<210> 23

<211> 184

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of a fusion protein comprising
GLP-1, helper peptide and β -galactosidase
protective peptide

<400> 23

Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Lys Asp
1 5 10 15
Trp Asp Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro
20 25 30
Pro Phe Ala Ser Trp Arg Asn Ser Asp Asp Ala Arg Thr Asp Arg Pro
35 40 45
Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg Phe Ala Trp Phe
50 55 60
Pro Ala Pro Glu Ala Val Pro Ala Ser Leu Leu Glu Ser Asp Leu Pro
65 70 75 80
Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr
85 90 95
Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro Ile Thr Val Asn Pro
100 105 110
Pro Phe Val Pro Thr Glu Pro His His His His His Gly Gly Arg Gln
115 120 125
Met His Gly Tyr Asp Ala Glu Leu Arg Leu Tyr Arg Arg His His Gly
130 135 140
Ser Gly Ser Pro Ser Arg His Pro Arg His Ala Glu Gly Thr Phe Thr
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Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile

165

170

175

Ala Trp Leu Val Lys Gly Arg Gly

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<210> 24

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence containing a site cleaved by
Kex2 Protease

<400> 24

Ser Cys His Lys Arg

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